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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds  
 (without alignments)  
 71.766 Million cell updates/sec

Title: US-09-787-443A-12  
 Perfect score: 11  
 Sequence: 1 ARQKTMKPRRS 11

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11  
 Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_29Jan04:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB	ID	Description
	Score	Match Length			
1	11	100.0	11	3 AAY88540	Aay88540 NCAM Igl
2	11	100.0	11	5 ABG69340	Abg69340 Human neu
3	4	36.4	11	2 AAR71762	Aar71762 Neurotens
4	4	36.4	11	2 AAR71761	Aar71761 Neurotens
5	4	36.4	11	4 AAB45669	Aab45669 Neurotens
6	4	36.4	11	6 AAE32335	Aae32335 Human vas
7	3	27.3	11	1 AAP50941	Aap50941 Hepatitis
8	3	27.3	11	1 AAP50942	Aap50942 Hepatitis
9	3	27.3	11	2 AAR05292	Aar05292 Amino aci

10	3	27.3	11	2	AAR14095	Aar14095	Pre-S(1-1
11	3	27.3	11	2	AAR14094	Aar14094	Pre-S(1-1
12	3	27.3	11	2	AAR24065	Aar24065	Cell-to-c
13	3	27.3	11	2	AAR28129	Aar28129	Cell-to-c
14	3	27.3	11	2	AAR28133	Aar28133	Cell-to-c
15	3	27.3	11	2	AAR24066	Aar24066	Cell-to-c
16	3	27.3	11	2	AAR28134	Aar28134	Cell-to-c
17	3	27.3	11	2	AAR28271	Aar28271	Cell-to-c
18	3	27.3	11	2	AAR24067	Aar24067	Cell-to-c
19	3	27.3	11	2	AAR28270	Aar28270	Cell-to-c
20	3	27.3	11	2	AAR28128	Aar28128	Cell-to-c
21	3	27.3	11	2	AAR28135	Aar28135	Cell-to-c
22	3	27.3	11	2	AAR28130	Aar28130	Cell-to-c
23	3	27.3	11	2	AAR24068	Aar24068	Cell-to-c
24	3	27.3	11	2	AAR28131	Aar28131	Cell-to-c
25	3	27.3	11	2	AAR28132	Aar28132	Cell-to-c
26	3	27.3	11	2	AAR44847	Aar44847	Lactoferr
27	3	27.3	11	2	AAR40877	Aar40877	SSP for f
28	3	27.3	11	2	AAR40874	Aar40874	SSP for f
29	3	27.3	11	2	AAR40878	Aar40878	SSP for f
30	3	27.3	11	2	AAR67084	Aar67084	Sweet pep
31	3	27.3	11	2	AAR71764	Aar71764	Neurotens
32	3	27.3	11	2	AAR71763	Aar71763	Neurotens
33	3	27.3	11	2	AAR52676	Aar52676	Fragment
34	3	27.3	11	2	AAR55785	Aar55785	Human car
35	3	27.3	11	2	AAR55788	Aar55788	Human car
36	3	27.3	11	2	AAR84118	Aar84118	Equine he
37	3	27.3	11	2	AAR79902	Aar79902	Human FK-
38	3	27.3	11	2	AAW21352	Aaw21352	Gastrin p
39	3	27.3	11	2	AAW21355	Aaw21355	Gastrin p
40	3	27.3	11	2	AAR73972	Aar73972	CD28 deri
41	3	27.3	11	2	AAR64665	Aar64665	HPF3 pept
42	3	27.3	11	2	AAR90612	Aar90612	Lactoferr
43	3	27.3	11	2	AAR87615	Aar87615	Lactoferr
44	3	27.3	11	2	AAW49555	Aaw49555	Human leu
45	3	27.3	11	2	AAR91858	Aar91858	Lactoferr
46	3	27.3	11	2	AAR96425	Aar96425	Hepatitis
47	3	27.3	11	2	AAR96424	Aar96424	Hepatitis
48	3	27.3	11	2	AAR96834	Aar96834	N.gonorrh
49	3	27.3	11	2	AAR96835	Aar96835	Human neu
50	3	27.3	11	2	AAW10520	Aaw10520	Lactoferr
51	3	27.3	11	2	AAW10518	Aaw10518	Lactoferr
52	3	27.3	11	2	AAW00844	Aaw00844	PERB11-4D
53	3	27.3	11	2	AAW24272	Aaw24272	Antifunga
54	3	27.3	11	2	AAW10445	Aaw10445	Human gro
55	3	27.3	11	2	AAW10434	Aaw10434	Human gro
56	3	27.3	11	2	AAW10451	Aaw10451	Human gro
57	3	27.3	11	2	AAW10433	Aaw10433	Human gro
58	3	27.3	11	2	AAW10459	Aaw10459	Human gro
59	3	27.3	11	2	AAW10441	Aaw10441	Human gro
60	3	27.3	11	2	AAW10453	Aaw10453	Human gro
61	3	27.3	11	2	AAW25322	Aaw25322	Peptide c
62	3	27.3	11	2	AAW25307	Aaw25307	Peptide c
63	3	27.3	11	2	AAW09807	Aaw09807	N-termina
64	3	27.3	11	2	AAW11150	Aaw11150	CD4 pepti
65	3	27.3	11	2	AAW39790	Aaw39790	Mammalian
66	3	27.3	11	2	AAW66283	Aaw66283	SMR1 pept

67	3	27.3	11	2	AAW53849	Aaw53849	Protein k
68	3	27.3	11	2	AAW38368	Aaw38368	Human pla
69	3	27.3	11	2	AAAY30260	Aay30260	KDR/Flk-1
70	3	27.3	11	2	AAAY30265	Aay30265	KDR/Flk-1
71	3	27.3	11	2	AAW96333	Aaw96333	Human ery
72	3	27.3	11	2	AAAY30081	Aay30081	A complem
73	3	27.3	11	2	AAAY45419	Aay45419	Immunogen
74	3	27.3	11	2	AAAY42687	Aay42687	HHV-6 var
75	3	27.3	11	2	AAW73368	Aaw73368	Human PAF
76	3	27.3	11	2	AAAY39668	Aay39668	Tat-inhib
77	3	27.3	11	2	AAAY33120	Aay33120	Zinc fing
78	3	27.3	11	2	AAAY25088	Aay25088	Transduct
79	3	27.3	11	2	AAAY25090	Aay25090	Transduct
80	3	27.3	11	2	AAAY25076	Aay25076	Transduct
81	3	27.3	11	2	AAAY25087	Aay25087	Transduct
82	3	27.3	11	2	AAAY25086	Aay25086	Transduct
83	3	27.3	11	2	AAAY07255	Aay07255	Lactoferr
84	3	27.3	11	3	AAAY78318	Aay78318	MMP prope
85	3	27.3	11	3	AAAY51589	Aay51589	HIV-1 der
86	3	27.3	11	3	AAAY68389	Aay68389	Rainbow t
87	3	27.3	11	3	AAAY93554	Aay93554	Amino aci
88	3	27.3	11	3	AAAY93552	Aay93552	Amino aci
89	3	27.3	11	3	AAAY93553	Aay93553	Amino aci
90	3	27.3	11	3	AAAY93556	Aay93556	Amino aci
91	3	27.3	11	3	AAAY93545	Aay93545	Amino aci
92	3	27.3	11	3	AAB14521	Aab14521	Sterile a
93	3	27.3	11	3	AAAY83526	Aay83526	Peptide f
94	3	27.3	11	3	AAB20662	Aab20662	Plasma HI
95	3	27.3	11	3	AAAY78450	Aay78450	Human gro
96	3	27.3	11	3	AAAY78444	Aay78444	Human gro
97	3	27.3	11	3	AAAY78437	Aay78437	Human gro
98	3	27.3	11	3	AAAY78456	Aay78456	Human gro
99	3	27.3	11	3	AAAY78442	Aay78442	Human gro
100	3	27.3	11	3	AAAY78433	Aay78433	Human gro

# ALIGNMENTS

## RESULT 1

AAAY88540

ID AAY88540 standard; peptide; 11 AA.

XX

AC AAY88540;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide #12.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 23-SEP-1999; 99WO-DK000500.  
XX  
PR 29-SEP-1998; 98DK-00001232.  
PR 29-APR-1999; 99DK-00000592.  
XX  
PA (RONN/) RONN L C B.  
PA (BOCK/) BOCK E.  
PA (HOLM/) HOLM A.  
PA (OLSE/) OLSEN M.  
PA (OSTE/) OSTERGAARD S.  
PA (JENS/) JENSEN P H.  
PA (POUL/) POULSEN F M.  
PA (SORO/) SOROKA V.  
PA (RALE/) RALETS I.  
PA (BERE/) BEREZIN V.  
XX  
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;  
PI Poulsen FM, Soroka V, Ralets I, Berezin V;  
XX  
DR WPI; 2000-293111/25.  
XX  
PT Compositions that bind neural cell adhesion molecules useful for treating  
PT disorders of the nervous system and muscles e.g. Alzheimer's and  
PT Parkinson's diseases.  
XX  
PS Example 4; Page 25; 119pp; English.  
XX  
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.  
CC NCAM is found in three forms, two of which are transmembrane forms, while  
CC the third is attached via a lipid anchor to the cell membrane. All three  
CC NCAM forms have an extracellular structure consisting five immunoglobulin  
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-  
CC terminal. The present sequence represents a peptide which binds to the  
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to  
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite  
CC outgrowth from NCAM presenting cells, and is also capable of promoting  
CC the proliferation of NCAM presenting cells. The compound may be used in  
CC the treatment of normal, degenerated or damaged NCAM presenting cells.  
CC The compound may in particular be used to treat diseases of the central  
CC and peripheral nervous systems such as post operative nerve damage,  
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions  
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,  
CC dementias, sclerosis, nerve degeneration associated with diabetes  
CC mellitus, disorders affecting the circadian clock or neuro-muscular  
CC transmission and schizophrenia. Conditions affecting the muscles may also  
CC be treated with the compound, such as conditions associated with impaired  
CC function of neuromuscular connections (e.g. genetic or traumatic shock or  
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas  
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,  
CC liver and bowel may also be treated using the compound. The compound is  
CC used in a prosthetic nerve guide, and also to stimulate the ability to  
CC learn, and to stimulate the memory of a subject  
XX



SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQKTMKPRRS 11  
| | | | | | | | | |  
Db 1 ARQKTMKPRRS 11

RESULT 2

ABG69340

ID ABG69340 standard; peptide; 11 AA.

XX

AC ABG69340;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #12.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,

PT in the preparation of medicament for preventing death of cells presenting

PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which

CC comprises at least 5 contiguous amino acid residues of a sequence of the

CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,

CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation  
 CC of a medicament for preventing death of cells presenting the NCAM or an  
 CC NCAM ligand. The medicament is for the stimulation of the survival of  
 CC heart muscle cells, such as survival after acute myocardial infarction.  
 CC The medicament is for the treatment of diseases or conditions of the  
 CC central and peripheral nervous system, such as postoperative nerve  
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,  
 CC impaired myelination of nerve fibres, postischaemic damage, e.g.  
 CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve  
 CC degeneration associated with diabetes mellitus, neuro-muscular  
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and  
 CC Huntington's disease. The medicament is for the treatment of diseases or  
 CC conditions of the muscles including conditions with impaired function of  
 CC neuro-muscular connections, such as genetic or traumatic atrophic muscle  
 CC disorders, and for the treatment of diseases or conditions of various  
 CC organs, such as degenerative conditions of the gonads, pancreas (e.g.  
 CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-  
 CC ABG69352 represent human NCAM peptides of the invention  
 XX  
 SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQKTMKPRRS 11  
 |||||  
 Db 1 ARQKTMKPRRS 11

# RESULT 3

AAR71762

ID AAR71762 standard; peptide; 11 AA.

XX

AC AAR71762;

XX

DT 25-MAR-2003 (revised)

DT 15-MAY-1995 (first entry)

XX

DE Neurotensin receptor fluorescent probe.

XX

KW Neurotensin; NT; receptor; probe; fluorescent.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Tyr or D-Tyr; and this residue is N-acylated with  
 FT fluorescent label. See CC below. Also this amino acid can  
 FT be substituted by Lys or Orn."

XX

PN EP606804-A2.

XX

PD 20-JUL-1994.

XX

PF 27-DEC-1993; 93EP-00403185.

XX

PR 30-DEC-1992; 92CA-02086453.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Beaudet A, Faure M, Gaudreau P;  
 XX  
 DR WPI; 1994-226757/28.  
 XX  
 PT New forescent markers for neurotensin receptors - useful for in vitro  
 PT labelling of neurotensin receptors on cell surface and to isolate  
 PT neurotensin-receptor expressing cells.  
 XX  
 PS Claim 2; Page 5; 19pp; English.  
 XX  
 CC The invention concerns highly sensitive fluorescent probes which allow  
 CC for rapid and precise characterisation of neurotensin receptor binding  
 CC properties on whole cells. The probes are of formula R1-C(=X)-R in which  
 CC R1 is is a fluorophore chosen from fluorescein, rhodamine, Blue  
 CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin  
 CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-  
 CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in  
 CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via  
 CC the N-terminus in position 1. The N-terminal amino acid may also be  
 CC substd. by Lys or Orn. The present sequence represents one of the claimed  
 CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPRR 10  
 ||||  
 Db 4 KPRR 7

#### RESULT 4

AAR71761

ID AAR71761 standard; peptide; 11 AA.

XX

AC AAR71761;

XX

DT 25-MAR-2003 (revised)

DT 15-MAY-1995 (first entry)

XX

DE Neurotensin receptor fluorescent probe.

XX

KW Neurotensin; NT; receptor; probe; fluorescent.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Tyr or D-Tyr; and this residue is N-acylated with  
 FT fluorescent label. See CC below. Also this amino acid can  
 FT be substituted by Lys or Orn."

XX  
 PN EP606804-A2.  
 XX  
 PD 20-JUL-1994.  
 XX  
 PF 27-DEC-1993; 93EP-00403185.  
 XX  
 PR 30-DEC-1992; 92CA-02086453.  
 XX  
 PA (UYMC-) UNIV MCGILL.  
 XX  
 PI Beaudet A, Faure M, Gaudreau P;  
 XX  
 DR WPI; 1994-226757/28.  
 XX  
 PT New forescent markers for neurotensin receptors - useful for in vitro  
 PT labelling of neurotensin receptors on cell surface and to isolate  
 PT neurotensin-receptor expressing cells.  
 XX  
 PS Claim 2; Page 5; 19pp; English.  
 XX  
 CC The invention concerns highly sensitive fluorescent probes which allow  
 CC for rapid and precise characterisation of neurotensin receptor binding  
 CC properties on whole cells. The probes are of formula R1-C(=X)-R in which  
 CC R1 is is a fluorophore chosen from fluorescein, rhodamine, Blue  
 CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin  
 CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-  
 CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in  
 CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via  
 CC the N-terminus in position 1. The N-terminal amino acid may also be  
 CC substd. by Lys or Orn. The present sequence represents one of the claimed  
 CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPRR 10  
 ||||  
 Db 4 KPRR 7

# RESULT 5

AAB45669

ID AAB45669 standard; peptide; 11 AA.

XX

AC AAB45669;

XX

DT 09-MAR-2001 (first entry)

XX

DE Neurotensin peptide analog #2.

XX

KW Vasoactive intestinal peptide; somatostatin; neurotensin; diagnosis;

KW polymethine dye; fluorescence; detection; tumor; adenoma; esophagus;

KW gastrointestinal tract; bronchial tract; bladder; cervix; breast;

KW optical mammography; optical tomography.  
 XX  
 OS Unidentified.  
 XX  
 PN DE19917713-A1.  
 XX  
 PD 19-OCT-2000.  
 XX  
 PF 09-APR-1999; 99DE-01017713.  
 XX  
 PR 09-APR-1999; 99DE-01017713.  
 XX  
 PA (DIAG-) INST DIAGNOSTIKFORSCHUNG GMBH.  
 XX  
 PI Licha K, Becker A, Semmler W, Wiedenmann B, Hessenius C;  
 PI Volkmer-Engert R, Schneider-Mergener J;  
 XX  
 DR WPI; 2001-000423/01.  
 XX  
 PT New conjugates of vasoactive intestinal peptide, somatostatin or  
 PT neurotensin peptides and polymethine dyes are used for e.g. in-vivo  
 PT fluorescence diagnosis of tumors and other diseased tissues.  
 XX  
 PS Claim 17; Page 17; 32pp; German.  
 XX  
 CC This invention describes novel conjugates (I) of vasoactive intestinal  
 CC peptide (VIP), somatostatin or neurotensin peptides and polymethine dyes.  
 CC The products of the invention can also be used for a diagnostic method  
 CC comprising administering (I) to a patient, either intravenously or to the  
 CC bronchi by inhalation or to the gastrointestinal tract, esophagus or  
 CC bladder by spraying and then washing out excess (I), and then performing  
 CC an endoscopic investigation by local excitation of fluorescence at an  
 CC excitation wavelength of 350-1200 nm and site-specific detection of the  
 CC fluorescence emitted by the dye. (I) are useful for in-vivo diagnosis of  
 CC tumors, other diseased tissues or adenomas by means of optical detection  
 CC procedures, in-vivo fluorescence diagnosis of tumors, tumor cells and/or  
 CC inflammatory tissues by means of endoscopic procedures in the  
 CC gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or  
 CC for in-vivo fluorescence and/or absorption diagnosis of breast tumors by  
 CC means of optical mammography (transillumination or optical tomography of  
 CC the breast). The peptide component provides receptor-specific binding to  
 CC target tissues and the polymethine dye provides a fluorescence signal  
 CC that is detectable with high sensitivity  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPRR 10  
 ||||  
 Db 5 KPRR 8

RESULT 6  
 AAE32335

ID AAE32335 standard; peptide; 11 AA.  
 XX  
 AC AAE32335;  
 XX  
 DT 24-MAR-2003 (first entry)  
 XX  
 DE Human vascular endothelial growth factor (VEGF) peptide #5.  
 XX  
 KW Vascular endothelial growth factor; VEGF; angiogenesis; wound healing;  
 KW bone growth; osteoporosis; osteoarthritis; bone reconstruction; ulcer;  
 KW lesion; injury; trauma; periodontal condition; protein therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283851-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US011406.  
 XX  
 PR 10-APR-2001; 2001US-00832355.  
 XX  
 PA (GENV-) GENVEC INC.  
 XX  
 PI Kovesdi I, Kessler PD;  
 XX  
 DR WPI; 2003-075536/07.  
 XX  
 PT New fusion protein comprising a non-heparin-binding vascular endothelial  
 PT growth factor (VEGF) peptide portion and a non-VEGF peptide portion,  
 PT useful for promoting angiogenesis and/or bone growth in mammals..  
 XX  
 PS Disclosure; Page 120; 191pp; English.  
 XX  
 CC The invention relates to a fusion protein comprising non-heparin binding  
 CC vascular endothelial growth factor (VEGF) peptide portion and a non-VEGF  
 CC peptide portion useful for promoting angiogenesis and/or bone growth in  
 CC mammalian host. The fusion protein is useful for promoting angiogenesis,  
 CC wound healing and bone growth. Compositions containing bone growth  
 CC promoting fusion protein can be used to treat osteoporosis, rheumatoid or  
 CC osteoarthritis, to improve poor bone healing, to promote implant  
 CC integration and function of artificial joints and to facilitate bone  
 CC reconstruction. They can also be used to treat e.g. ulcers, lesions,  
 CC injuries, burns, trauma, periodontal conditions, lacerations and other  
 CC conditions. The invention is also useful in protein therapy. The present  
 CC sequence is human VEGF peptide  
 XX  
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10  
 ||||  
 Db 8 KPRR 11

RESULT 7

AAP50941

ID AAP50941 standard; peptide; 11 AA.

XX

AC AAP50941;

XX

DT 25-MAR-2003 (revised)

DT 06-OCT-1991 (first entry)

XX

DE Hepatitis B virus (HBV) envelope protein pre-S gene peptide fragment.

XX

KW Immunogen; vaccine; antigen; epitope; diagnosis.

XX

OS Hepatitis B virus.

XX

PN EP154902-A.

XX

PD 18-SEP-1985.

XX

PF 28-FEB-1985; 85EP-00102250.

XX

PR 07-MAR-1984; 84US-00587090.

PR 05-FEB-1985; 85US-00698499.

PR 28-APR-1986; 86US-00856522.

XX

PA (CALY ) CALIFORNIA INST OF TECHN.

PA (NYBL-) NEW YORK BLOOD CENTER INC.

XX

PI Neurath AR, Kent SBH;

XX

DR WPI; 1985-237979/39.

XX

PT Pre-s gene coded hepatitis B immunogens - useful in in vaccines for protection and as diagnostics for detection of antigens and antigens.

XX

PS Claim 30; Page 101; 140pp; English.

XX

CC The peptides of the invention are immunogens which, esp. when linked to carriers, may be used in vaccines for conferring protection against HBV, and in the diagnosis of viral conditions in man and animals and in the detection of the antigens and antibodies. More specifically, the chain of CC AAs is between sequence posn. pre-S 120-174. (Updated on 25-MAR-2003 to CC correct PA field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9

|||

Db 7 KPR 9

RESULT 8

AAP50942

ID AAP50942 standard; peptide; 11 AA.

XX

AC AAP50942;

XX

DT 25-MAR-2003 (revised)

DT 06-OCT-1991 (first entry)

XX

DE Hepatitis B virus (HBV) envelope protein pre-S gene peptide fragment.

XX

KW Immunogen; vaccine; antigen; epitope; diagnosis.

XX

OS Hepatitis B virus.

XX

PN EP154902-A.

XX

PD 18-SEP-1985.

XX

PF 28-FEB-1985; 85EP-00102250.

XX

PR 07-MAR-1984; 84US-00587090.

PR 05-FEB-1985; 85US-00698499.

PR 28-APR-1986; 86US-00856522.

XX

PA (CALY ) CALIFORNIA INST OF TECHN.

PA (NYBL-) NEW YORK BLOOD CENTER INC.

XX

PI Neurath AR, Kent SBH;

XX

DR WPI; 1985-237979/39.

XX

PT Pre-s gene coded hepatitis B immunogens - useful in in vaccines for  
PT protection and as diagnostics for detection of antigens and antigens.

XX

PS Claim 31; Page 101; 140pp; English.

XX

CC The peptides of the invention are immunogens which, esp. when linked to  
CC carriers, may be used in vaccines for conferring protection against HBV,  
CC and in the diagnosis of viral conditions in man and animals and in the  
CC detection of the antigens and antibodies. More specifically, the chain of  
CC AAs is between sequence posn. pre-S 120-174. (Updated on 25-MAR-2003 to  
CC correct PA field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9

|||

Db 7 KPR 9

RESULT 9

AAR05292

ID AAR05292 standard; protein; 11 AA.



XX  
 AC AAR05292;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 03-AUG-1990 (first entry)  
 XX  
 DE Amino acid sequence encoded by modified portion of new synthetic human  
 DE lymphotoxin (HL) gene.  
 XX  
 KW Synthetic human lymphotoxin (HL) gene.  
 XX  
 OS Homo sapiens.  
 XX  
 PN JP02000447-A.  
 XX  
 PD 05-JAN-1990.  
 XX  
 PF 13-NOV-1987; 87JP-00287035.  
 XX  
 PR 27-OCT-1987; 87JP-00271513.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 1990-047988/07.  
 DR N-PSDB; AAQ93388, AAQ93372.  
 XX  
 PT Human lymphotoxin synthetic gene - is altered to leave only one side of  
 PT restriction enzyme recognition site, etc.  
 XX  
 PS Disclosure; Fig 4; 13pp; Japanese.  
 XX  
 CC It is the amino acid sequence of a modified portion of the new synthetic  
 CC human lymphotoxin gene. The gene has been engineered so that  
 CC modifications such as those carried out on its DNA are easier to produce.  
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
 CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
 |||  
 Db 1 ARQ 3

# RESULT 10

AAR14095

ID AAR14095 standard; protein; 11 AA.  
 XX  
 AC AAR14095;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 04-DEC-1991 (first entry)  
 XX

DE Pre-S(1-11) immunogenic peptide based on HBV subtype adr.  
 XX  
 KW hepatitis B virus; vaccine; liposome-peptide complex.  
 XX  
 OS Synthetic.  
 XX  
 PN EP448126-A.  
 XX  
 PD 25-SEP-1991.  
 XX  
 PF 28-FEB-1985; 91EP-00105948.  
 XX  
 PR 07-MAR-1984; 84US-00587090.  
 PR 05-FEB-1985; 85US-00698499.  
 XX  
 PA (NYBL-) NEW YORK BLOOD CENTER INC.  
 PA (CALY ) CALIFORNIA INST OF TECHN.  
 XX  
 PI Neurath AR, Kent SBH;  
 XX  
 DR WPI; 1991-283144/39.  
 XX  
 PT Synthetic lipid vesicle carrier linked to pre-S gene coded peptide - the  
 PT peptide is a hepatitis B immunogen, vaccine or diagnostic.  
 XX  
 PS Disclosure; Page 13; 54pp; English.  
 XX  
 CC This peptide is one of ten preferred HBV antigenic sequences which are  
 CC suitable for attachment to lipid vesicles for use as vaccines. The lipid  
 CC vesicle carrier is stabilised by cross-linking and has covalently bonded  
 CC sites on its outer surface to bind the peptide. See also AAR14086-R14094.  
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
 CC correct PA field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
 |||  
 Db 7 KPR 9

RESULT 11

AAR14094

ID AAR14094 standard; protein; 11 AA.

XX

AC AAR14094;

XX

DT 25-MAR-2003 (revised)

DT 04-DEC-1991 (first entry)

XX

DE Pre-S(1-11) immunogenic peptide based on HBV subtype adw2.

XX

KW hepatitis B virus; vaccine; liposome-peptide complex.

XX  
 OS Synthetic.  
 XX  
 PN EP448126-A.  
 XX  
 PD 25-SEP-1991.  
 XX  
 PF 28-FEB-1985; 91EP-00105948.  
 XX  
 PR 07-MAR-1984; 84US-00587090.  
 PR 05-FEB-1985; 85US-00698499.  
 XX  
 PA (NYBL-) NEW YORK BLOOD CENTER INC.  
 PA (CALY ) CALIFORNIA INST OF TECHN.  
 XX  
 PI Neurath AR, Kent SBH;  
 XX  
 DR WPI; 1991-283144/39.  
 XX  
 PT Synthetic lipid vesicle carrier linked to pre-S gene coded peptide - the  
 PT peptide is a hepatitis B immunogen, vaccine or diagnostic.  
 XX  
 PS Disclosure; Page 13; 54pp; English.  
 XX  
 CC This peptide is one of ten preferred HBV antigenic sequences which are  
 CC suitable for attachment to lipid vesicles for use as vaccines. The lipid  
 CC vesicle carrier is stabilised by cross-linking and has covalently bonded  
 CC sites on its outer surface to bind the peptide. See AAR14086-R14095.  
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to  
 CC correct PA field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
 |||  
 Db 7 KPR 9

# RESULT 12

AAR24065

ID AAR24065 standard; protein; 11 AA.

XX

AC AAR24065;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (4).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers  
 FT Cross-links 4. .11  
 FT /note= "sequence linked by interchain disulfide bonds  
 FT with Cys residue on Arg3-Cys-Arg2-Ser-Arg-Gly-Asp-Val"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Claim 67; Page 69; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins may comprise two subunits having the sequence below, held  
 CC together by an interchain stable bond. The sequence RGD is in each of the  
 CC subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 13

AAR28129

ID AAR28129 standard; protein; 11 AA.

XX

AC AAR28129;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (17).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 4. .11  
 FT /note= "sequence linked by interchain amide bond at Lys  
 FT position to Glu residue on Arg3-Glu-Arg2-Ser-Arg-Gly-Asp-  
 FT Val sequence (see AAR28128)"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Disclosure; Page 40-41; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequences given in AAR28128-  
 CC 29, held together by an interchain stable bond. The sequence RGD is in  
 CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11  
 |||  
 Db 5 RRS 7

#### RESULT 14

AAR28133

ID AAR28133 standard; protein; 11 AA.

XX

AC AAR28133;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (21).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 2. .11  
 FT /note= "sequence linked by interchain amide bond at Lys  
 FT position to Glu residue on Arg-Glu-Arg4-Ser-Arg-Gly-Asp-  
 FT Val sequence (see AAR28132)"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Disclosure; Page 43-44; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequences given in AAR28132-  
 CC 33, held together by an interchain stable bond. The sequence RGD is in  
 CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 15

AAR24066

ID AAR24066 standard; protein; 11 AA.

XX

AC AAR24066;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (5).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 3. .11  
 FT /note= "multimers of sequence linked by interchain  
 FT disulfide bonds with Cys residues"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Claim 67; Page 69; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins may comprise two subunits having the sequence below, held  
 CC together by an interchain stable bond. The sequence RGD is in each of the  
 CC subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 16

AAR28134

ID AAR28134 standard; protein; 11 AA.

XX

AC AAR28134;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (22).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 1. .11

FT /note= "sequence linked by interchain amide bond at Glu  
FT position to Lys residue on Lys-Arg5-Ser-Arg-Gly-Asp-Val  
FT sequence (see AAR28135)"  
XX

PN WO9208476-A1.  
XX

PD 29-MAY-1992.  
XX

PF 07-NOV-1991; 91WO-US008328.  
XX

PR 07-NOV-1990; 90US-00610363.  
XX

PA (SCRI ) SCRIPPS RES INST.  
XX

PI Ruggeri ZM, Houghten RA;  
XX

DR WPI; 1992-199940/24.  
XX

PT Peptides inhibiting binding of adhesion mols. to cells expressing  
PT integrins - for treating and preventing thrombus formation and diseases  
PT associated with platelet aggregation.  
XX

PS Disclosure; Page 44-45; 70pp; English.  
XX

CC A peptide which inhibits binding of adhesion mols. to cells expressing  
CC integrins comprises two subunits having the sequences given in AAR28134-  
CC 35, held together by an interchain stable bond. The sequence RGD is in  
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11

|||

Db 5 RRS 7

#### RESULT 17

AAR28271

ID AAR28271 standard; protein; 11 AA.  
XX

AC AAR28271;  
XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)  
XX

DE Cell-to-cell binding inhibiting peptide subunit (39).  
XX

KW Adhesion; integrin; multimer.  
XX

OS Synthetic.  
XX

FH Key Location/Qualifiers

FT Cross-links 11



FT /note= "sequence linked by interchain amide bond at X=ORN  
 FT to Glu residue on Arg3-Cys-Arg2-Ser-Arg-Gly-Asp-Glu  
 FT sequence (see AAR28271)"  
 FT Modified-site 11  
 FT /label= ORN  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Disclosure; Page 61-62; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequences given in AAR28270-  
 CC 71, held together by an interchain stable bond. The sequence RGD is in  
 CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 18

AAR24067

ID AAR24067 standard; protein; 11 AA.

XX

AC AAR24067;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (6).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers  
 FT Cross-links 2. .11  
 FT /note= "multimers of sequence linked by interchain  
 FT disulfide bonds with Cys residues"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Claim 67; Page 69; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins may comprise two subunits having the sequence below, held  
 CC together by an interchain stable bond. The sequence RGD is in each of the  
 CC subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 19

AAR28270

ID AAR28270 standard; protein; 11 AA.

XX

AC AAR28270;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (38).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 11. .11  
 FT /note= "sequence linked by interchain amide bond at Glu  
 FT position to Orn residue on Arg3-Cys-Arg2-Ser-Arg-Gly-Asp-  
 FT Orn sequence (see AAR28271)"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Disclosure; Page 61-62; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequences given in AAR28270-  
 CC 71, held together by an interchain stable bond. The sequence RGD is in  
 CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 20

AAR28128

ID AAR28128 standard; protein; 11 AA.

XX

AC AAR28128;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (16).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 4. .11  
 FT /note= "sequence linked by interchain amide bond at Glu  
 FT position to Lys residue on Arg3-Lys-Arg2-Ser-Arg-Gly-Asp-  
 FT Val sequence (see AAR28129)"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Disclosure; Page 40-41; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequences given in AAR28128-  
 CC 29, held together by an interchain stable bond. The sequence RGD is in  
 CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 21

AAR28135

ID AAR28135 standard; protein; 11 AA.

XX

AC AAR28135;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (23).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 1. .11  
 FT /note= "sequence linked by interchain amide bond at Lys  
 FT position to Glu residue on Glu-Arg5-Ser-Arg-Gly-Asp-Val  
 FT sequence (see AAR28133)"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Disclosure; Page 44-45; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequences given in AAR28134-  
 CC 35, held together by an interchain stable bond. The sequence RGD is in  
 CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 22

AAR28130

ID AAR28130 standard; protein; 11 AA.

XX

AC AAR28130;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (18).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 3. .11  
 FT /note= "sequence linked by interchain amide bond at Glu  
 FT position to Lys residue on Arg2-Lys-Arg3-Ser-Arg-Gly-Asp-  
 FT Val sequence (see AAR28131)"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Disclosure; Page 41-43; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequences given in AAR28130-  
 CC 31, held together by an interchain stable bond. The sequence RGD is in  
 CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 23

AAR24068

ID AAR24068 standard; protein; 11 AA.

XX

AC AAR24068;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (7).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 1. .11  
 FT /note= "multimers of sequence linked by interchain  
 FT disulfide bonds with Cys residues"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Claim 67; Page 70; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequence below, held together  
 CC by an interchain stable bond. The sequence RGD is in each of the  
 CC subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 5 RRS 7

#### RESULT 24

AAR28131

ID AAR28131 standard; protein; 11 AA.

XX

AC AAR28131;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (19).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 3. .11

FT /note= "sequence linked by interchain amide bond at Lys  
FT position to Glu residue on Arg2-Glu-Arg3-Ser-Arg-Gly-Asp-  
FT Val sequence (see AAR28130)"

XX

PN WO9208476-A1.

XX

PD 29-MAY-1992.

XX

PF 07-NOV-1991; 91WO-US008328.

XX

PR 07-NOV-1990; 90US-00610363.

XX

PA (SCRI ) SCRIPPS RES INST.

XX

PI Ruggeri ZM, Houghten RA;

XX

DR WPI; 1992-199940/24.

XX

PT Peptides inhibiting binding of adhesion mols. to cells expressing  
PT integrins - for treating and preventing thrombus formation and diseases  
PT associated with platelet aggregation.

XX

PS Disclosure; Page 41-43; 70pp; English.

XX

CC A peptide which inhibits binding of adhesion mols. to cells expressing  
CC integrins comprises two subunits having the sequences given in AAR28130-  
CC 31, held together by an interchain stable bond. The sequence RGD is in  
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11

|||

Db 5 RRS 7

RESULT 25

AAR28132

ID AAR28132 standard; protein; 11 AA.

XX

AC AAR28132;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (20).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 2. .11



FT /note= "sequence linked by interchain amide bond at Glu  
 FT position to Lys residue on Arg-Lys-Arg4-Ser-Arg-Gly-Asp-  
 FT Val sequence (see AAR28133)"  
 XX  
 PN WO9208476-A1.  
 XX  
 PD 29-MAY-1992.  
 XX  
 PF 07-NOV-1991; 91WO-US008328.  
 XX  
 PR 07-NOV-1990; 90US-00610363.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Ruggeri ZM, Houghten RA;  
 XX  
 DR WPI; 1992-199940/24.  
 XX  
 PT Peptides inhibiting binding of adhesion mols. to cells expressing  
 PT integrins - for treating and preventing thrombus formation and diseases  
 PT associated with platelet aggregation.  
 XX  
 PS Disclosure; Page 43-44; 70pp; English.  
 XX  
 CC A peptide which inhibits binding of adhesion mols. to cells expressing  
 CC integrins comprises two subunits having the sequences given in AAR28132-  
 CC 33, held together by an interchain stable bond. The sequence RGD is in  
 CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 5 RRS 7

# RESULT 26

AAR44847

ID AAR44847 standard; peptide; 11 AA.

XX

AC AAR44847;

XX

DT 25-MAR-2003 (revised)

DT 09-JAN-2003 (revised)

DT 31-JAN-1994 (first entry)

XX

DE Lactoferrin-related antibacterial peptide.

XX

KW Lactoferrin; antibiotic; chelate; mastitis; bowel disorder; disease;

KW bacteria; yeast; fungi; disinfection; drug; foodstuff; cosmetic;

KW toiletries.

XX

OS Unidentified.

XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 10  
 FT /note= "Cys10 forms disulfide bond with Cys35 of sequence  
 FT in AAR44846"  
 XX  
 PN WO9314640-A1.  
 XX  
 PD 05-AUG-1993.  
 XX  
 PF 30-NOV-1992; 92WO-JP001563.  
 XX  
 PR 23-JAN-1992; 92JP-00032660.  
 PR 11-MAR-1992; 92JP-00052943.  
 PR 30-SEP-1992; 92JP-00262143.  
 PR 30-SEP-1992; 92JP-00262559.  
 XX  
 PA (MORG ) MORINAGA MILK IND CO LTD.  
 XX  
 PI Tomita M, Shimamura S, Kawase K, Fukuwatari Y, Takase M;  
 PI Bellamy W, Yamauchi K, Wakabayashi H, Tokita Y;  
 XX  
 DR WPI; 1993-258265/32.  
 XX  
 PT Antibacterial agent comprising decomposition products of lactoferrin -  
 PT with chelate e.g. EDTA alcohol and/or antibiotic e.g. penicillin, also  
 PT useful against yeast and fungi.  
 XX  
 PS Disclosure; Page 88; 100pp; Japanese.  
 XX  
 CC Lactoferrin-related peptides are used in new antibacterial compsn. The  
 CC compsn. is highly effective against a broad range of bacteria, yeasts and  
 CC fungi. It can be used therapeutically (internal and external  
 CC application), e.g. for mastitis, bowel disorders, urinary infections,  
 CC etc. It can also be used for the disinfection and protection of drugs,  
 CC foodstuffs, cosmetics and toiletries and household items (such as kitchen  
 CC towels and toilet paper). (Updated on 09-JAN-2003 to add missing OS  
 CC field.) (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 4 RRS 6

RESULT 27  
 AAR40877  
 ID AAR40877 standard; protein; 11 AA.  
 XX  
 AC AAR40877;  
 XX  
 DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)  
 DT 28-MAR-1994 (first entry)  
 XX  
 DE SSP for flavonoid-3',5'-hydroxylase gene product.  
 XX  
 KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;  
 KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;  
 KW polymerase chain reaction; amplification; expression; ss.  
 XX  
 OS Petunia x hybrida.  
 XX  
 PN WO9318155-A1.  
 XX  
 PD 16-SEP-1993.  
 XX  
 PF 20-NOV-1992; 92WO-JP001520.  
 XX  
 PR 02-MAR-1992; 92JP-00044963.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX  
 PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;  
 PI Okinaka Y;  
 XX  
 DR WPI; 1993-303469/38.  
 DR N-PSDB; AAQ47878.  
 XX  
 PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to  
 PT transform plants e.g. petunia, rose or tobacco to give bluer flower  
 PT colour and altered pigment pattern.  
 XX  
 PS Claim 11; Page 58; 82pp; Japanese.  
 XX  
 CC Insertion of the sequences (AAQ47840-42) into plants such as rose,  
 CC petunia, tobacco and carnation, using a suitable vector such as  
 CC agrobacterium, give transformed plants which express the gene, resulting  
 CC in petals with a bluer colour than normal, and/or pigmentation patterns  
 CC which do not occur naturally. The sequences were amplified using primers  
 CC (AAQ47843-70). Related single specific primers using a gene sequence  
 CC coding for the haem-binding region of cytochrome P450 are shown in  
 CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated  
 CC on 24-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
 |||  
 Db 6 PRR 8

RESULT 28  
 AAR40874  
 ID AAR40874 standard; protein; 11 AA.

XX  
 AC AAR40874;  
 XX  
 DT 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 28-MAR-1994 (first entry)  
 XX  
 DE SSP for flavonoid-3',5'-hydroxylase gene.  
 XX  
 KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;  
 KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;  
 KW polymerase chain reaction; amplification; expression; ss.  
 XX  
 OS Petunia x hybrida.  
 XX  
 PN WO9318155-A1.  
 XX  
 PD 16-SEP-1993.  
 XX  
 PF 20-NOV-1992; 92WO-JP001520.  
 XX  
 PR 02-MAR-1992; 92JP-00044963.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.  
 XX  
 PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;  
 PI Okinaka Y;  
 XX  
 DR WPI; 1993-303469/38.  
 DR N-PSDB; AAQ47875.  
 XX  
 PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to  
 PT transform plants e.g. petunia, rose or tobacco to give bluer flower  
 PT colour and altered pigment pattern.  
 XX  
 PS Claim 11; Page 57; 82pp; Japanese.  
 XX  
 CC Insertion of the sequences (AAQ47840-42) into plants such as rose,  
 CC petunia, tobacco and carnation, using a suitable vector such as  
 CC agrobacterium, give transformed plants which express the gene, resulting  
 CC in petals with a bluer colour than normal, and/or pigmentation patterns  
 CC which do not occur naturally. The sequences were amplified using primers  
 CC (AAQ47843-70). Related single specific primers using a gene sequence  
 CC coding for the haem-binding region of cytochrome P450 are shown in  
 CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated  
 CC on 24-OCT-2003 to standardise OS field)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 6 RRS 8

RESULT 29

AAR40878

ID AAR40878 standard; protein; 11 AA.

XX

AC AAR40878;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-MAR-1994 (first entry)

XX

DE SSP for flavonoid-3',5'-hydroxylase gene product.

XX

KW Flavonoid-3',5'-hydroxylase; transformation; plants; petunia; rose;  
KW tobacco; pigment alteration; blue; SSP; single specific primer; PCR;  
KW polymerase chain reaction; amplification; expression.

XX

OS Petunia x hybrida.

XX

PN WO9318155-A1.

XX

PD 16-SEP-1993.

XX

PF 20-NOV-1992; 92WO-JP001520.

XX

PR 02-MAR-1992; 92JP-00044963.

XX

PA (KYOW ) KYOWA HAKKO KOGYO CO LTD.

XX

PI Kikuchi Y, Kiyokawa S, Shimada Y, Ohbayashi M, Shimada R;

PI Okinaka Y;

XX

DR WPI; 1993-303469/38.

DR N-PSDB; AAQ47879.

XX

PT Gene coding for flavonoid-3',5'-hydroxylase of petunia petals - used to  
PT transform plants e.g. petunia, rose or tobacco to give bluer flower  
PT colour and altered pigment pattern.

XX

PS Claim 11; Page 58; 82pp; Japanese.

XX

CC Insertion of the sequences (AAQ47840-42) into plants such as rose,  
CC petunia, tobacco and carnation, using a suitable vector such as  
CC agrobacterium, give transformed plants which express the gene, resulting  
CC in petals with a bluer colour than normal, and/or pigmentation patterns  
CC which do not occur naturally. The sequences were amplified using primers  
CC (AAQ47843-70). Related single specific primers using a gene sequence  
CC coding for the haem-binding region of cytochrome P450 are shown in  
CC (AAQ47871-Q47903). (Updated on 25-MAR-2003 to correct PN field.) (Updated  
CC on 24-OCT-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 6 RRS 8

RESULT 30

AAR67084

ID AAR67084 standard; peptide; 11 AA.

XX

AC AAR67084;

XX

DT 25-MAR-2003 (revised)

DT 29-JUN-1995 (first entry)

XX

DE Sweet peptide (SW-MB1) contg. proline brackets.

XX

KW Sweet peptide; non-nutrient sweetner; food; drink; dessert; candy;

KW interaction site; constrained conformation; reduce calorie intake;

KW sweet tasting papillae; diabetes; mimic; thaumatin; monellin; mabinlin.

XX

OS Synthetic.

XX

PN WO9425482-A1.

XX

PD 10-NOV-1994.

XX

PF 21-APR-1994; 94WO-US004294.

XX

PR 23-APR-1993; 93US-00051741.

PR 29-OCT-1993; 93US-00143364.

XX

PA (EVAN/) EVANS H J.

PA (KINI/) KINI R M.

XX

PI Evans HJ, Kini RM;

XX

DR WPI; 1994-358186/44.

XX

PT Peptide homologue or analogue with constrained conformation - has proline  
PT residues flanking the interaction site to impart greater, or more stable,  
PT biological activity.

XX

PS Example 2; Page 32; 57pp; English.

XX

CC AAR67077-88 are sweet peptides derived from naturally occurring  
CC polypeptides that contain proline or proline/cysteine brackets. These  
CC peptides are shortened to form fragments that contain one or more  
CC interaction sites of interest. AAR67084-88 are deriv. from mabinlin. The  
CC sweet peptides bind to receptors of sweet tasting papillae and induce a  
CC sweet sensation. Typically, these peptides are 5000 to 10000 times  
CC sweeter than sugar. In comparison, aspartame is only 160 times sweeter  
CC than sugar. The peptides are useful as non-nutrient sweeteners for food,  
CC etc. and are helpful in normal and low calorie diets. They are esp.  
CC suitable for people with diabetes. The data collected demonstrates that  
CC interaction sites possess activity when present in a polypeptide that  
CC differs from the native form. Inclusion of conformation-constraining  
CC moieties can have desirable effects on an interaction site. (Also see

CC AAR67011-76 and AAR67089-152 for analogues of other biologically active  
CC peptides contg. an interaction site flanked by conformation constraining  
CC gps., eg. RGD peptides.) (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 2 PRR 4

RESULT 31  
AAR71764

ID AAR71764 standard; peptide; 11 AA.

XX

AC AAR71764;

XX

DT 25-MAR-2003 (revised)

DT 15-MAY-1995 (first entry)

XX

DE Neurotensin receptor fluorescent probe.

XX

KW Neurotensin; NT; receptor; probe; fluorescent.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Tyr or D-Tyr; and this residue is N-acylated with  
FT fluorescent label. See CC below. Also this amino acid can  
FT be substituted by Lys or Orn."

FT Modified-site 4

FT /label= Orn

XX

PN EP606804-A2.

XX

PD 20-JUL-1994.

XX

PF 27-DEC-1993; 93EP-00403185.

XX

PR 30-DEC-1992; 92CA-02086453.

XX

PA (UYMC-) UNIV MCGILL.

XX

PI Beaudet A, Faure M, Gaudreau P;

XX

DR WPI; 1994-226757/28.

XX

PT New fluorescent markers for neurotensin receptors - useful for in vitro  
PT labelling of neurotensin receptors on cell surface and to isolate  
PT neurotensin-receptor expressing cells.

XX

PS Claim 2; Page 5; 19pp; English.

XX  
 CC The invention concerns highly sensitive fluorescent probes which allow  
 CC for rapid and precise characterisation of neurotensin receptor binding  
 CC properties on whole cells. The probes are of formula R1-C(=X)-R in which  
 CC R1 is is a fluorophore chosen from fluorescein, rhodamine, Blue  
 CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin  
 CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-  
 CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in  
 CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via  
 CC the N-terminus in position 1. The N-terminal amino acid may also be  
 CC substd. by Lys or Orn. The present sequence represents one of the claimed  
 CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
 |||  
 Db 5 PRR 7

# RESULT 32

AAR71763

ID AAR71763 standard; peptide; 11 AA.

XX

AC AAR71763;

XX

DT 25-MAR-2003 (revised)

DT 15-MAY-1995 (first entry)

XX

DE Neurotensin receptor fluorescent probe.

XX

KW Neurotensin; NT; receptor; probe; fluorescent.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Tyr or D-Tyr; and this residue is N-acylated with  
 FT fluorescent label. See CC below. Also this amino acid can  
 FT be substituted by Lys or Orn."

FT Modified-site 4

FT /label= Orn

XX

PN EP606804-A2.

XX

PD 20-JUL-1994.

XX

PF 27-DEC-1993; 93EP-00403185.

XX

PR 30-DEC-1992; 92CA-02086453.

XX

PA (UYMC-) UNIV MCGILL.

XX



PI Beaudet A, Faure M, Gaudreau P;  
 XX  
 DR WPI; 1994-226757/28.  
 XX  
 PT New forescent markers for neurotensin receptors - useful for in vitro  
 PT labelling of neurotensin receptors on cell surface and to isolate  
 PT neurotensin-receptor expressing cells.  
 XX  
 PS Claim 2; Page 5; 19pp; English.  
 XX  
 CC The invention concerns highly sensitive fluorescent probes which allow  
 CC for rapid and precise characterisation of neurotensin receptor binding  
 CC properties on whole cells. The probes are of formula R1-C(=X)-R in which  
 CC R1 is is a fluorophore chosen from fluorescein, rhodamine, Blue  
 CC fluorescent and Texas red; X is oxygen or sulphur; and R is a neurotensin  
 CC -type polypeptide sequence containing the core sequence Arg-Arg-Pro-Tyr-  
 CC Ile-Leu or Arg-Arg-Pro-Trp-Ile-Leu. Specific sequences are given in  
 CC AAR71745 - AAR71772. The R1-CX- acyl group is linked to the peptide via  
 CC the N-terminus in position 1. The N-terminal amino acid may also be  
 CC substd. by Lys or Orn. The present sequence represents one of the claimed  
 CC peptide sequences for R. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRR 10  
 III  
 Db 5 PRR 7

RESULT 33  
 AAR52676

ID AAR52676 standard; protein; 11 AA.  
 XX  
 AC AAR52676;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 09-AUG-1994 (first entry)  
 XX  
 DE Fragment encoded by homology vector used to inactivate herpesvirus.  
 XX  
 KW Equine herpesvirus; US2; vaccine; antigen; protection; prophylaxis;  
 KW prevention; vector.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9403628-A1.  
 XX  
 PD 17-FEB-1994.  
 XX  
 PF 06-AUG-1993; 93WO-US007424.  
 XX  
 PR 07-AUG-1992; 92US-00926784.

XX  
PA (SYTR ) SYNTRO CORP.  
XX  
PI Cochran MD;  
XX  
DR WPI; 1994-065715/08.  
DR N-PSDB; AAQ56623.  
XX  
PT New recombinant equine herpes viruses - used to prepare vaccines to  
PT protect horses from infectious equine herpes virus.  
XX  
PS Disclosure; Fig 7; 153pp; English.  
XX  
CC Recombinant equine herpesvirus' (EHV) have a foreign DNA sequence  
CC inserted into their genomes. The inserted sequence is a piece of foreign,  
CC double stranded DNA which encodes an RNA molecule which does not  
CC naturally occur in the animal into which the EHV is introduced. The  
CC foreign DNA sequence is introduced into the EHV via a homology vector.  
CC The recombinant EHV's are used to prepare vaccines to protect horses from  
CC infectious EHV. This sequence is encoded by a fragment of a homology  
CC vector. A desired DNA fragment can be cloned into the homology vector.  
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to  
CC correct OS field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 4 PRR 6

# RESULT 34

AAR55785

ID AAR55785 standard; peptide; 11 AA.

XX

AC AAR55785;

XX

DT 25-MAR-2003 (revised)

DT 21-FEB-1995 (first entry)

XX

DE Human cardiac troponin I N-terminal sequence (16-26).

XX

KW Human cardiac troponin I; heart muscle necrosis; immunogen; epitope;

KW immunodiagnosis; acute myocardial infarction.

XX

OS Homo sapiens.

XX

PN DE4243648-A1.

XX

PD 07-JUL-1994.

XX

PF 23-DEC-1992; 92DE-04243648.

XX

PR 23-DEC-1992; 92DE-04243648.  
 XX  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 XX  
 PI Lill H, Donie F, Borgya A, Seidel C;  
 XX  
 DR WPI; 1994-218764/27.  
 XX  
 PT Rapid diagnosis of heart muscle necrosis in myocardial infarction - by  
 PT immunological test using new antibody recognising cardiac troponin I N-  
 PT terminal peptide.  
 XX  
 PS Claim 2; Page 10; 12pp; German.  
 XX  
 CC The N-terminal 30 amino acids of human cardiac troponin I (AAR55781) or  
 CC subfragments of it (AAR55782-R55788) can be used as immunogens. The  
 CC antibodies raised by immunising animals (pref. sheep) with the peptides  
 CC are useful for rapid diagnosis of heart muscle necrosis. (Updated on 25-  
 CC MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 6 RRS 8

RESULT 35  
 AAR55788

ID AAR55788 standard; peptide; 11 AA.  
 XX  
 AC AAR55788;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-FEB-1995 (first entry)  
 XX  
 DE Human cardiac troponin I N-terminal sequence (16-26).  
 XX  
 KW Human cardiac troponin I; heart muscle necrosis; immunogen; epitope;  
 KW immunodiagnosis; acute myocardial infarction.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE4243648-A1.  
 XX  
 PD 07-JUL-1994.  
 XX  
 PF 23-DEC-1992; 92DE-04243648.  
 XX  
 PR 23-DEC-1992; 92DE-04243648.  
 XX  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 XX

PI Lill H, Donie F, Borgya A, Seidel C;  
 XX  
 DR WPI; 1994-218764/27.  
 XX  
 PT Rapid diagnosis of heart muscle necrosis in myocardial infarction - by  
 PT immunological test using new antibody recognising cardiac troponin 1 N-  
 PT terminal peptide.  
 XX  
 PS Claim 2; Page 11; 12pp; German.  
 XX  
 CC The N-terminal 30 amino acids of human cardiac troponin I (AAR55781) or  
 CC subfragments of it (AAR55782-R55788) can be used as immunogens. The  
 CC antibodies raised by immunising animals (pref. sheep) with the peptides  
 CC are useful for rapid diagnosis of heart muscle necrosis. (Updated on 25-  
 CC MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11  
 |||  
 Db 6 RRS 8

RESULT 36

AAR84118

ID AAR84118 standard; peptide; 11 AA.

XX

AC AAR84118;

XX

DT 22-MAR-1996 (first entry)

XX

DE Equine herpesvirus (EHV4) glycoprotein H residues 288-298.

XX

KW Equine herpesvirus 4; EHV4; recombinant; vaccine; attenuated virus;

KW diagnosis; plasmid 495-61.39; junction C; glycoprotein H.

XX

OS Synthetic.

XX

PN WO9522607-A1.

XX

PD 24-AUG-1995.

XX

PF 16-FEB-1995; 95WO-US002087.

XX

PR 17-FEB-1994; 94US-00198094.

XX

PA (SYTR ) SYNTRO CORP.

XX

PI Cochran MD, Chiang CH;

XX

DR WPI; 1995-302714/39.

DR N-PSDB; AAT00545.

XX

PT Recombinant equine herpes viruses pref. contg. a deletion in a region not  
PT essential for replication - used in vaccines to protect horses from  
PT infection.

XX

PS Example 5; Fig 7; 159pp; English.

XX

CC AAR84118 is encoded by the equine herpesvirus 4 (EHV) plasmid 495-61.39  
CC junction C. The plasmid was used in the construction of a recombinant  
CC attenuated EHV. The attenuated virus can be used as a foetal safe vaccine  
CC to protect an equine against EHV, or in a test to determine if an equine  
CC has been vaccinated against or is infected with EHV

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10

|||

Db 4 PRR 6

#### RESULT 37

AAR79902

ID AAR79902 standard; peptide; 11 AA.

XX

AC AAR79902;

XX

DT 19-MAR-1996 (first entry)

XX

DE Human FK-506 cytosolic binding protein FKBP12 residues 38-48.

XX

KW Human; cytosolic binding protein; FKBP12; residues 38-48; FK-506;  
KW diagnosis; purification; determination; detection; immunosuppressant;  
KW binding partner; antibodies.

XX

OS Homo sapiens.

XX

PN WO9521861-A1.

XX

PD 17-AUG-1995.

XX

PF 10-FEB-1995; 95WO-US001721.

XX

PR 15-FEB-1994; 94US-00197795.

XX

PA (MERI ) MERCK & CO INC.

XX

PI Wiederrecht GJ, Sewell TJ;

XX

DR WPI; 1995-293076/38.

XX

PT New FK-506 cytosolic binding protein - used for diagnostic, purification  
PT or investigational procedures, partic. for detection of FK-506.

XX

PS Disclosure; Page 9; 68pp; English.

XX  
CC AAR79900-R79902 are peptides from the human FK-506 immunosuppressant  
CC cytosolic binding protein FKBP12. The peptides were conjugated to  
CC thyroglobulin, and used to generate anti-peptide antibodies. The  
CC antibodies were used to survey tissue and cell extracts relevant to the  
CC immunosuppressive effects FK-506. FKBP12 can be used as a specific  
CC binding partner for a variety of ligands for diagnostic, purifcn. and  
CC investigatory procedures. It can also be used to determine the presence  
CC or quantity of FK-506 in a sample, e.g. a body fluid from an  
CC immunosuppressed individual on FK-506 therapy

XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQK 4  
|||  
Db 5 RQK 7

RESULT 38

AAW21352

ID AAW21352 standard; peptide; 11 AA.

XX

AC AAW21352;

XX

DT 29-JUL-1997 (first entry)

XX

DE Gastrin precursor derived signal oligopeptide #10.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;  
KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;  
KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;  
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;  
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;  
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;  
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Homo sapiens.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX  
 DR WPI; 1995-263953/34.  
 XX  
 PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PT regions of max. hydrophilicity, used in modulating communication between  
 PT protein(s).  
 XX  
 PS Claim 5; Page 48; 88pp; English.  
 XX  
 CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface of the  
 CC protein and are represented by the hydrophilicity maxima of the protein.  
 CC These peptides are enriched in charged amino acids arranged with neutral  
 CC spacer amino acids. The specific signal character of these oligopeptides  
 CC is determined by a characteristic combination of conformation and charge  
 CC within the signal sequence. These oligopeptides may be used as vaccines  
 CC in the treatment of human disease, as competitive inhibitors to prevent  
 CC or reduce the metabolic action or interaction of a selected protein by  
 CC blocking its specific signal sequences, or as therapeutic agents to  
 CC function as feedback regulators to reduce synthesis rate of a selected  
 CC protein. These peptides may be modified by omitting one or more amino  
 CC acids at the N- and/or C-terminal, by substituting one or more amino  
 CC acids without consideration of charge and polarity, by substituting one  
 CC or more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 4 RRS 6

# RESULT 39

AAW21355

ID AAW21355 standard; peptide; 11 AA.

XX

AC AAW21355;

XX

DT 29-JUL-1997 (first entry)

XX

DE Gastrin precursor derived signal oligopeptide #13.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;  
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;  
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;  
 KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;  
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;  
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;  
 KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;  
 KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;

KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9519568-A1.  
 XX  
 PD 20-JUL-1995.  
 XX  
 PF 12-JAN-1995; 95WO-US000575.  
 XX  
 PR 14-JAN-1994; 94US-00182248.  
 XX  
 PA (RATH/) RATH M.  
 XX  
 PI Rath M;  
 XX  
 DR WPI; 1995-263953/34.  
 XX  
 PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as  
 PT regions of max. hydrophilicity, used in modulating communication between  
 PT protein(s).  
 XX  
 PS Claim 5; Page 48; 88pp; English.  
 XX  
 CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are localised on the surface of the  
 CC protein and are represented by the hydrophilicity maxima of the protein.  
 CC These peptides are enriched in charged amino acids arranged with neutral  
 CC spacer amino acids. The specific signal character of these oligopeptides  
 CC is determined by a characteristic combination of conformation and charge  
 CC within the signal sequence. These oligopeptides may be used as vaccines  
 CC in the treatment of human disease, as competitive inhibitors to prevent  
 CC or reduce the metabolic action or interaction of a selected protein by  
 CC blocking its specific signal sequences, or as therapeutic agents to  
 CC function as feedback regulators to reduce synthesis rate of a selected  
 CC protein. These peptides may be modified by omitting one or more amino  
 CC acids at the N- and/or C-terminal, by substituting one or more amino  
 CC acids without consideration of charge and polarity, by substituting one  
 CC or more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11  
 III  
 Db 1 RRS 3

RESULT 40  
 AAR73972  
 ID AAR73972 standard; peptide; 11 AA.  
 XX  
 AC AAR73972;



XX  
 DT 13-DEC-1995 (first entry)  
 XX  
 DE CD28 derived competitive peptide.  
 XX  
 KW Inhibitor; CD28; phosphatidyl inositol 3-kinase; PI3-kinase; immune;  
 KW response; autoimmune disease.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 4  
 FT /note= "opt. phosphorylated."  
 XX  
 PN WO9510628-A2.  
 XX  
 PD 20-APR-1995.  
 XX  
 PF 09-SEP-1994; 94WO-US010090.  
 XX  
 PR 28-SEP-1993; 93US-00128971.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 XX  
 PI Rudd CE, Kanteti P;  
 XX  
 DR WPI; 1995-161812/21.  
 XX  
 PT Modulating signal transduction in T cells - by modifying the association  
 PT of CD28 with phosphatidyl:inositol 3-kinase to alter immune response.  
 XX  
 PS Disclosure; Page 14; 5lpp; English.  
 XX  
 CC AAR73971 and AAR73972 are derived from Polyoma virus middle-T antigen.  
 CC They are used in peptide competition experiments to determine the  
 CC importance of the CD28 PI3-kinase binding motif Tyr-Met-X-Met. By  
 CC introducing into a T cell a peptide of the cytoplasmic tail of CD28, the  
 CC association of phosphatidyl inositol (PI) 3-kinase and CD28 can be  
 CC reduced. This results in a lowered immune response and is useful in the  
 CC treatment of autoimmune diseases e.g. systemic lupus erythematosus, type  
 CC 1 diabetes and rheumatoid arthritis, it is also useful in preventing the  
 CC rejection of transplanted organs and cells  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
 |||  
 Db 9 PRR 11

RESULT 41

AAR64665

ID AAR64665 standard; peptide; 11 AA.

XX  
 AC AAR64665;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 04-SEP-1995 (first entry)  
 XX  
 DE HPF3 peptide derivative 42, from anti-human parainfluenza virus.  
 XX  
 KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;  
 KW human immunodeficiency virus; transmembrane protein; gp41; HPF3;  
 KW anti-human parainfluenza virus.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "optionally has an amino, acetyl, 9-  
 FT fluorenylmethoxy-carbonyl, hydrophobic or macromolecular  
 FT carrier gp. attached"  
 FT Modified-site 11  
 FT /note= "optionally has a carboxyl, amido, hydrophobic or  
 FT macromolecular carrier gp. attached"  
 XX  
 PN WO9428920-A1.  
 XX  
 PD 22-DEC-1994.  
 XX  
 PF 07-JUN-1994; 94WO-US005739.  
 XX  
 PR 07-JUN-1993; 93US-00073028.  
 XX  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM;  
 PI Petteway SR;  
 XX  
 DR WPI; 1995-036105/05.  
 XX  
 PT Computer search generated synthetic peptides - are inhibitors of HIV  
 PT transmission.  
 XX  
 PS Claim 15; Page 140; 182pp; English.  
 XX  
 CC AAR64657-88 are peptide derivatives of a 35 mer HPF3 peptide derived from  
 CC anti-human parainfluenza virus (AAR64656) which have been truncated at  
 CC the amino terminus. The peptides are DP-178 like peptides. DP-178  
 CC corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI  
 CC transmembrane protein gp41. It forms a putative alpha helix at the C-  
 CC terminal end of the gp41 ectodomain, and complexes with DP-107  
 CC (corresponds to amino acids 558-595) which contains a leucine zipper  
 CC motif. The peptides complex via non-covalent protein-protein  
 CC interactions. The peptide derivatives were identified by a computer  
 CC assisted peptide sequence search. The antiviral activity of this peptide  
 CC is not stated in the specification. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 9 RRS 11

RESULT 42

AAR90612

ID AAR90612 standard; peptide; 11 AA.

XX

AC AAR90612;

XX

DT 10-JUL-1996 (first entry)

XX

DE Lactoferrin derived peptide #28.

XX

KW Lactoferrin; antitumour; therapy; tumour; parenteral administration;

KW thermostable; cytotoxic; antibacterial.

XX

OS Synthetic.

XX

PN JP07309771-A.

XX

PD 28-NOV-1995.

XX

PF 17-MAY-1994; 94JP-00103109.

XX

PR 17-MAY-1994; 94JP-00103109.

XX

PA (MORG ) MORINAGA MILK IND CO LTD.

XX

DR WPI; 1996-045317/05.

XX

PT Antitumour agent, derived from lactoferrin, for parenteral administration

PT - has few side effects and is thermally stable and water soluble.

XX

PS Claim 1; Page 10; 10pp; Japanese.

XX

CC AAR90585-R90613 represent lactoferrin derived peptides. These sequences  
CC can be used as antitumour agents for parenteral administration. The  
CC sequences are thermally stable, water soluble and stable in water. These  
CC peptide sequences are only cytotoxic to tumour cells. Administration of  
CC these sequences results in few side effects. No antiseptic is required  
CC for administration due to the antibacterial action of the peptide. Drugs  
CC made from these peptides can be rapidly metabolised

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11

Db                    |||  
                      4 RRS 6

RESULT 43

AAR87615

ID    AAR87615 standard; peptide; 11 AA.

XX

AC    AAR87615;

XX

DT    11-JUL-1996    (first entry)

XX

DE    Lactoferrin-derived anti-fungal peptide.

XX

KW    Anti-fungal; water soluble; lactoferrin; stable; anti-bacterial;  
KW    rapidly metabolised.

XX

OS    Synthetic.

XX

FH    Key                    Location/Qualifiers

FT    Disulfide-bond    9

FT                                /note= "forms disulphide bond with Cys at position 35 of  
FT                                peptide AAR87626"

XX

PN    JP07309774-A.

XX

PD    28-NOV-1995.

XX

PF    17-MAY-1994;    94JP-00126882.

XX

PR    17-MAY-1994;    94JP-00126882.

XX

PA    (MORG ) MORINAGA MILK IND CO LTD.

XX

DR    WPI; 1996-045320/05.

XX

PT    Water-soluble anti-fungus agent derived from lactoferrin - has  
PT    antibacterial action and is not cytotoxic to animal cells.

XX

PS    Claim 1; Page 10; 11pp; Japanese.

XX

CC    AAR87599-R87627 are the active ingredients of an anti-fungal agent. The  
CC    agent has anti-bacterial as well as anti-fungal properties but is only  
CC    cytotoxic to fungal cells. The agent is water-soluble, hence drugs made  
CC    from the agent are rapidly metabolised. The peptides are derived from  
CC    fragmented lactoferrin

XX

SQ    Sequence 11 AA;

Query Match                    27.3%;    Score 3;    DB 2;    Length 11;

Best Local Similarity    100.0%;    Pred. No. 8.3e+03;

Matches        3;    Conservative        0;    Mismatches        0;    Indels        0;    Gaps        0;

Qy                    9 RRS 11

|||

Db                    4 RRS 6

RESULT 44

AAW49555

ID AAW49555 standard; peptide; 11 AA.

XX

AC AAW49555;

XX

DT 05-JUN-1998 (first entry)

XX

DE Human leucocyte antigen DQ4 binding peptide #446.

XX

KW Human leucocyte antigen; HLA-DQ4; combinatorial library;

KW autoimmune disease; chronic articular rheumatism.

XX

OS Synthetic.

XX

PN JP08151396-A.

XX

PD 11-JUN-1996.

XX

PF 28-NOV-1994; 94JP-00292657.

XX

PR 28-NOV-1994; 94JP-00292657.

XX

PA (TEIJ ) TEIJIN LTD.

XX

DR WPI; 1996-329479/33.

XX

PT HLA-binding oligopeptide and an immuno:regulator contg it - used in the  
PT treatment of auto:immune disease.

XX

PS Claim 4; Page 49; 6lpp; Japanese.

XX

CC This peptide is an example of a peptide which binds to a human leucocyte  
CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
CC combinatorial library comprising the sequence AAV05953, by screening with  
CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune  
CC disease, or especially for treatment of viral diseases

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3

|||

Db 5 ARQ 7

RESULT 45

AAR91858

ID AAR91858 standard; peptide; 11 AA.

XX

AC AAR91858;

XX

DT 20-SEP-1996 (first entry)

XX  
DE Lactoferrin-derived specific peptide, useful for wound healing.  
XX  
KW Bovine lactoferrin; wound healing; skin damage; burn; bedsore;  
KW heterodimer; intermolecular disulphide bond.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Cross-links 10  
FT /label= disulphide  
FT /note= "forms disulphide bond with Cys35 of peptide  
FT sequence given in AAR91857"  
XX  
PN JP08081387-A.  
XX  
PD 26-MAR-1996.  
XX  
PF 09-SEP-1994; 94JP-00241894.  
XX  
PR 09-SEP-1994; 94JP-00241894.  
XX  
PA (MORG ) MORINAGA MILK IND CO LTD.  
XX  
DR WPI; 1996-217187/22.  
XX  
PT Wound healing agent comprising specific peptide(s) - is heat resistant,  
PT stable in aqueous solution and suitable for oral, external or  
PT subcutaneous admin.  
XX  
PS Claim 1; Page 11; 12pp; Japanese.  
XX  
CC The present peptide is useful in a novel wound healing agent. The agent  
CC is thermostable and stable in aqueous solution. It is administered  
CC externally, orally or subcutaneously for treatment of skin damage such as  
CC burns or bedsores  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
| | |  
Db 4 RRS 6

RESULT 46  
AAR96425  
ID AAR96425 standard; peptide; 11 AA.  
XX  
AC AAR96425;  
XX  
DT 07-MAR-1997 (first entry)  
XX  
DE Hepatitis C virus type 1d peptide #2.

XX  
 KW Hepatitis C virus; subtype; polymerase chain reaction; amplification;  
 KW PCR; primer; probe; antibody; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9613590-A2.  
 XX  
 PD 09-MAY-1996.  
 XX  
 PF 23-OCT-1995; 95WO-EP004155.  
 XX  
 PR 21-OCT-1994; 94EP-00870166.  
 PR 28-JUN-1995; 95EP-00870076.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Maertens G, Stuyver L;  
 XX  
 DR WPI; 1996-251460/25.  
 XX  
 PT Hepatitis C virus poly:nucleic acid unique to unidentified sub:type -  
 PT used to develop probes and primers for new sub:types and vaccines to  
 PT prevent and treat infection.  
 XX  
 PS Claim 5; Page 65; 150pp; English.  
 XX  
 CC The peptides AAR96424-R96524 represent novel peptides derived from the  
 CC novel hepatitis C virus subtypes 1d-f, 2e-i, 2k, 2l, 3g, 4k-m, 7a-c or  
 CC types 9, 10 or 11 (see AAT27937-T27989). The sequences corresp. to the 5'  
 CC untranslated region (UR), the Core/E1, NS4 or NS5B regions of the genome.  
 CC This sequence is from the HCV subtype 1d. The new HCV types were isolated  
 CC from patients with chronic HCV from the Benelux countries, France,  
 CC Cameroon and Vietnam, because of their aberrant reactivities. The RNA was  
 CC extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The  
 CC 5'UR, Core/E1 and NS5B regions were sequenced either directly or  
 CC partially and used to classify the new viruses into (sub)types based on  
 CC comparison with known sequences. The nucleotide sequences can be used to  
 CC synthesise probes and primers for the detection of HCV in a sample. The  
 CC polypeptides can be used to detect anti-HCV antibodies, for HCV typing or  
 CC to prevent HCV infections  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 2 RRS 4

#### RESULT 47

AAR96424

ID AAR96424 standard; peptide; 11 AA.

XX

AC AAR96424;  
 XX  
 DT 07-MAR-1997 (first entry)  
 XX  
 DE Hepatitis C virus type 1d peptide #1.  
 XX  
 KW Hepatitis C virus; subtype; polymerase chain reaction; amplification;  
 KW PCR; primer; probe; antibody; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9613590-A2.  
 XX  
 PD 09-MAY-1996.  
 XX  
 PF 23-OCT-1995; 95WO-EP004155.  
 XX  
 PR 21-OCT-1994; 94EP-00870166.  
 PR 28-JUN-1995; 95EP-00870076.  
 XX  
 PA (INNO-) INNOGENETICS NV.  
 XX  
 PI Maertens G, Stuyver L;  
 XX  
 DR WPI; 1996-251460/25.  
 XX  
 PT Hepatitis C virus poly:nucleic acid unique to unidentified sub:type -  
 PT used to develop probes and primers for new sub:types and vaccines to  
 PT prevent and treat infection.  
 XX  
 PS Claim 5; Page 65; 150pp; English.  
 XX  
 CC The peptides AAR96424-R96524 represent novel peptides derived from the  
 CC novel hepatitis C virus subtypes 1d-f, 2e-i, 2k, 2l, 3g, 4k-m, 7a-c or  
 CC types 9, 10 or 11 (see AAT27937-T27989). The sequences corresp. to the 5'  
 CC untranslated region (UR), the Core/E1, NS4 or NS5B regions of the genome.  
 CC This sequence is from the HCV subtype 1d. The new HCV types were isolated  
 CC from patients with chronic HCV from the Benelux countries, France,  
 CC Cameroon and Vietnam, because of their aberrant reactivities. The RNA was  
 CC extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The  
 CC 5'UR, Core/E1 and NS5B regions were sequenced either directly or  
 CC partially and used to classify the new viruses into (sub)types based on  
 CC comparison with known sequences. The nucleotide sequences can be used to  
 CC synthesise probes and primers for the detection of HCV in a sample. The  
 CC polypeptides can be used to detect anti-HCV antibodies, for HCV typing or  
 CC to prevent HCV infections  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARQ 3  
 |||  
 Db 1 ARQ 3



RESULT 48

AAR96834

ID AAR96834 standard; peptide; 11 AA.

XX

AC AAR96834;

XX

DT 16-OCT-2003 (revised)

DT 29-NOV-1996 (first entry)

XX

DE N.gonorrhoeae Iga alphal region, homologous to human Nfh protein.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;

KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;

KW human neurofilament triplet h protein; Nfh.

XX

OS Neisseria gonorrhoeae; MS11.

XX

FH Key Location/Qualifiers

FT Region 1. .3

FT /note= "identical to sequence in human neurofilament

FT triplet h protein"

FT Region 5. .7

FT /note= "identical to sequence in human neurofilament

FT triplet h protein"

FT Region 10. .11

FT /note= "identical to sequence in human neurofilament

FT triplet h protein"

XX

PN WO9609395-A2.

XX

PD 28-MAR-1996.

XX

PF 21-SEP-1995; 95WO-EP003726.

XX

PR 21-SEP-1994; 94DE-04433708.

XX

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX

PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;

PI Oetzelberger KB;

XX

DR WPI; 1996-188456/19.

XX

PT Medicaments for treating auto-immune or viral diseases - contg.

PT substances interfering with bacterial poly:protein function.

XX

PS Claim 32; Fig 2; 117pp; German.

XX

CC The present sequence is a cleavage product from the Iga alpha 1 domain of  
 CC the precursor of IgA-protease polyprotein (IPP) of N.gonorrhoeae strain  
 CC MS11. The Neisseria IPP has marked homology to certain human proteins and  
 CC has been implicated in rheumatoid arthritis and other auto-immune  
 CC diseases. The polyprotein also activates proviruses, including HIV.  
 CC Substances which interfere with the function of IPP from Neisseria will  
 CC be useful for treating associated autoimmune diseases and viral  
 CC infections. The present peptide is homologous to a region from human

CC neurofilament triplet h protein. (Updated on 16-OCT-2003 to standardise  
CC OS field)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 1 ARQ 3

RESULT 49

AAR96835

ID AAR96835 standard; peptide; 11 AA.

XX

AC AAR96835;

XX

DT 29-NOV-1996 (first entry)

XX

DE Human neurofilament triplet h fragment, homologous to Neisseria Iga-  
DE alpha1.

XX

KW IgA protease precursor; IPP; bacterial polyprotein; autoimmune;  
KW viral infection; rheumatoid arthritis; AIDS; meningococcal bacteria;  
KW human neurofilament triplet h protein; Nfh; Neisseria gonorrhoeae; MS11.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .3

FT /note= "identical to sequence in Neisseria gonorrhoeae  
FT Iga-alpha1"

FT Region 5. .7

FT /note= "identical to sequence in Neisseria gonorrhoeae  
FT Iga-alpha1"

FT Region 10. .11

FT /note= "identical to sequence in Neisseria gonorrhoeae  
FT Iga-alpha1"

XX

PN WO9609395-A2.

XX

PD 28-MAR-1996.

XX

PF 21-SEP-1995; 95WO-EP003726.

XX

PR 21-SEP-1994; 94DE-04433708.

XX

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX

PI Meyer TF, Pohlner J, Beck SC, Jose J, Woelk U, Lorenzen DR;  
PI Oetzelberger KB;

XX

DR WPI; 1996-188456/19.

XX

PT Medicaments for treating auto-immune or viral diseases - contg.  
PT substances interfering with bacterial poly:protein function.  
XX  
PS Claim 32; Fig 2; 117pp; German.  
XX  
CC The present sequence from human neurofilament triplet h protein has  
CC homology to a cleavage product from the Iga-alpha1 domain of the  
CC precursor of IgA-protease polyprotein (IPP) of Neisseria gonorrhoeae  
CC strain MS11. The Neisseria IPP has been implicated in rheumatoid  
CC arthritis and other auto-immune diseases. The polyprotein also activates  
CC proviruses, including HIV. Substances which interfere with the function  
CC of IPP from Neisseria will be useful for treating associated autoimmune  
CC diseases and viral infections. Peptides comprising the homology region  
CC sequences, whether from Neisseria or from humans, are claimed  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
| | |  
Db 1 ARQ 3

# RESULT 50

AAW10520

ID AAW10520 standard; peptide; 11 AA.

XX

AC AAW10520;

XX

DT 02-APR-1997 (first entry)

XX

DE Lactoferrin derived antibacterial peptide.

XX

KW Lactoferrin; antibacterial; immunogen; monoclonal; antibody; human;

KW bovine; hybridoma; sensitive; specific; detection; determination;

KW gastric juice; intestine; faeces; blood; urine.

XX

OS Synthetic.

XX

PN JP08269099-A.

XX

PD 15-OCT-1996.

XX

PF 30-MAR-1995; 95JP-00073177.

XX

PR 30-MAR-1995; 95JP-00073177.

XX

PA (MORG ) MORINAGA MILK IND CO LTD.

XX

DR WPI; 1996-515017/51.

XX

PT Monoclonal antibody combined with bovine or non-natural human lactoferrin

PT fragment - for detecting lactoferrin-originated antibacterial peptide in

PT e.g. gastric juice, urine etc.

XX  
 PS Claim 3; Page 12; 13pp; Japanese.  
 XX  
 CC The present peptide is a lactoferrin (LF) derived antibacterial peptide,  
 CC which can be used as an immunogen in the prepn. of a monoclonal antibody  
 CC (MAb), capable of binding with a human or bovine LF fragment but not with  
 CC natural LF, using standard hybridoma techniques. The MAb can be used for  
 CC the highly sensitive and specific detection or determination of LF  
 CC derived antibacterial peptides in gastric juice, intestinal contents,  
 CC faeces, blood and urine  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 4 RRS 6

RESULT 51  
 AAW10518  
 ID AAW10518 standard; peptide; 11 AA.  
 XX  
 AC AAW10518;  
 XX  
 DT 02-APR-1997 (first entry)  
 XX  
 DE Lactoferrin derived antibacterial dimeric peptide.  
 XX  
 KW Lactoferrin; antibacterial; immunogen; monoclonal; antibody; human;  
 KW bovine; hybridoma; sensitive; specific; detection; determination;  
 KW gastric juice; intestine; faeces; blood; urine; dimer.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Cross-links 10  
 FT /note= "disulfide bonded to Cys 35 of AAW10517"  
 XX  
 PN JP08269099-A.  
 XX  
 PD 15-OCT-1996.  
 XX  
 PF 30-MAR-1995; 95JP-00073177.  
 XX  
 PR 30-MAR-1995; 95JP-00073177.  
 XX  
 PA (MORG ) MORINAGA MILK IND CO LTD.  
 XX  
 DR WPI; 1996-515017/51.  
 XX  
 PT Monoclonal antibody combined with bovine or non-natural human lactoferrin  
 PT fragment - for detecting lactoferrin-originated antibacterial peptide in  
 PT e.g. gastric juice, urine etc.

XX  
 PS Claim 3; Page 12; 13pp; Japanese.  
 XX  
 CC The present peptide is a lactoferrin (LF) derived dimeric antibacterial  
 CC peptide, which can be used as an immunogen in the prepn. of a monoclonal  
 CC antibody (MAb), capable of binding with a human or bovine LF fragment but  
 CC not with natural LF, using standard hybridoma techniques. The MAb can be  
 CC used for the highly sensitive and specific detection or determination of  
 CC LF derived antibacterial peptides in gastric juice, intestinal contents,  
 CC faeces, blood and urine  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 4 RRS 6

# RESULT 52

AAW00844

ID AAW00844 standard; peptide; 11 AA.

XX

AC AAW00844;

XX

DT 30-DEC-1996 (first entry)

XX

DE PERB11-4D peptide.

XX

KW PERB11 gene; major histocompatibility complex; MHC; polymorphism;

KW haplotype; vaccine; therapy; diagnosis; psoriasis;

KW nasopharyngeal carcinoma; spondyloarthropathy; myasthenia gravis; IgAd;

KW CVI; cerebral malaria; rheumatoid arthritis; AIDS; cachexia.

XX

OS Synthetic.

XX

PN WO9630511-A1.

XX

PD 03-OCT-1996.

XX

PF 29-MAR-1996; 96WO-AU000184.

XX

PR 29-MAR-1995; 95AU-00002014.

PR 29-MAR-1995; 95AU-00002015.

XX

PA (IMMU-) IMMUNOGENETICS RES FOUND INC.

XX

PI Dawkins RL;

XX

DR WPI; 1996-455358/45.

XX

PT Sequences relevant to MHC associated disease - used for vaccine

PT preparation and diagnosis of, e.g. Psoriasis, Nasopharyngeal carcinoma(s)

PT and Spondyloarthropathies and Myasthenia gravis.

XX  
 PS Claim 17; Page 52; 94pp; English.  
 XX  
 CC Peptides PERB11-4D (AAW00844) and PERB11-5D (AAW05276) are located within  
 CC the alpha-1 domain of PERB11.1 proteins (see also AAW00839-43) from 5  
 CC major histocompatibility complex (MHC) ancestral haplotypes; peptide  
 CC PERB11-6D (AAW05277) is located in the alpha-2 domain. PERB11 is a  
 CC polymorphic gene family (see also AAT39575-78) with multiple copies  
 CC within the MHC. Antibodies raised against the PERB11 peptides can be used  
 CC to identify and purify proteins related to MHC-associated diseases  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQK 4  
 |||  
 Db 3 RQK 5

# RESULT 53

AAW24272

ID AAW24272 standard; peptide; 11 AA.

XX

AC AAW24272;

XX

DT 15-OCT-1997 (first entry)

XX

DE Antifungal peptide #8, derived from lactoferrin.

XX

KW Lactoferrin; hydrolysis; antifungal agent; hydrolysate; food;

KW azole-type anti-fungal compound; dermatophytosis; dermatomycosis.

XX

OS Synthetic.

XX

PN JP09165342-A.

XX

PD 24-JUN-1997.

XX

PF 14-DEC-1995; 95JP-00347405.

XX

PR 14-DEC-1995; 95JP-00347405.

XX

PA (MORG ) MORINAGA MILK IND CO LTD.

XX

DR WPI; 1997-381279/35.

XX

PT Antifungal agents containing azole(s) and lactoferrin hydrolysate - for

PT treatment of dermatophytosis and dermatomycosis.

XX

PS Claim 4; Page 10; 10pp; Japanese.

XX

CC The sequences given in AAW24265-72 are peptides which are derived from  
 CC lactoferrin by hydrolysis. These peptides may be used in the antifungal  
 CC agents of the invention which also contain as the active component an

CC azole-type anti-fungal compound. The antifungal agents are used for  
CC treatment of dermatophytosis and dermatomycosis. The antifungal agents of  
CC this invention show the same as or higher effect at one quarter to one  
CC sixteenth the dose of known antifungal compounds, so the dose of these  
CC compounds having adverse reactions can be reduced. Lactoferrin  
CC hydrolysates have no toxicity since they have been used as a part of food  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 4 RRS 6

RESULT 54

AAW10445

ID AAW10445 standard; peptide; 11 AA.

XX

AC AAW10445;

XX

DT 25-MAR-2003 (revised)

DT 11-AUG-1997 (first entry)

XX

DE Human growth hormone Leu-73 substitution peptide.

XX

KW Active site; active domain; growth hormone; somatogenic receptor;  
KW mutagenesis.

XX

OS Synthetic.

XX

PN US5580723-A.

XX

PD 03-DEC-1996.

XX

PF 02-FEB-1994; 94US-00190723.

XX

PR 28-OCT-1988; 88US-00264611.

PR 26-OCT-1989; 89US-00428066.

PR 27-APR-1992; 92US-00875204.

PR 13-OCT-1992; 92US-00960227.

XX

PA (GETH ) GENENTECH INC.

XX

PI Cunningham BC, Wells JA;

XX

DR WPI; 1997-033563/03.

XX

PT Identification of unknown active domains in polypeptide(s) - useful for  
PT analysis of structure and function of hormones, etc.

XX

PS Disclosure; Col 26; 86pp; English.

XX

CC Substitution peptides (AAW10441-62) were used to identify specific amino

CC acid residues in human growth hormone (hGH) (AAW10425) which are expected  
CC to product hGH variants having altered biological functions. The method  
CC involved substituting selected amino acid segments of hGH with analogous  
CC segments from analogue polypeptides (human placenta lactogen, human  
CC prolactin and pig growth hormone) and examining the effect of the  
CC substns. on interaction with the soluble hGH receptor (see also  
CC AAW10426). Once active site domains had been detd., amino acid residues  
CC within these domains were replaced sequentially with alanine, and the  
CC effects on interaction with the hGH receptor were again examined. Leu-73  
CC was identified by this method; the preferred amino acid substn. for this  
CC residue is given in AAW10445. Active site residues have also been  
CC identified (see also AAW10427-40). (Updated on 25-MAR-2003 to correct PF  
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARQ 3

|||

Db 5 ARQ 7

#### RESULT 55

AAW10434

ID AAW10434 standard; peptide; 11 AA.

XX

AC AAW10434;

XX

DT 25-MAR-2003 (revised)

DT 11-AUG-1997 (first entry)

XX

DE Human growth hormone active site Lys-172 substitution peptide.

XX

KW Active site; active domain; growth hormone; somatogenic receptor;

KW mutagenesis.

XX

OS Synthetic.

XX

PN US5580723-A.

XX

PD 03-DEC-1996.

XX

PF 02-FEB-1994; 94US-00190723.

XX

PR 28-OCT-1988; 88US-00264611.

PR 26-OCT-1989; 89US-00428066.

PR 27-APR-1992; 92US-00875204.

PR 13-OCT-1992; 92US-00960227.

XX

PA (GETH ) GENENTECH INC.

XX

PI Cunningham BC, Wells JA;

XX

DR WPI; 1997-033563/03.



XX  
PT Identification of unknown active domains in polypeptide(s) - useful for  
PT analysis of structure and function of hormones, etc.  
XX  
PS Disclosure; Col 24; 86pp; English.  
XX  
CC Substitution peptides (AAW10427-40) were used to identify active site  
CC amino acids within active domains of human growth hormone (hGH)  
CC (AAW10425). The method involved substituting selected amino acid segments  
CC of hGH with analogous segments from analogue polypeptides (human placenta  
CC lactogen, human prolactin and pig growth hormone) and examining the  
CC effect of the substns. on interaction with the soluble hGH receptor (see  
CC also AAW10426). Once active site domains had been detd., amino acid  
CC residues within these domains were replaced sequentially with alanine,  
CC and the effects on interaction with the hGH receptor were again examined.  
CC Lys-172 was identified as an active site residue by this method; the  
CC preferred amino acid substn. for this residue is given in AAW10434.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
| | |  
Db 5 ARQ 7

# RESULT 56

AAW10451

ID AAW10451 standard; peptide; 11 AA.

XX

AC AAW10451;

XX

DT 25-MAR-2003 (revised)

DT 11-AUG-1997 (first entry)

XX

DE Human growth hormone Asn-99 substitution peptide.

XX

KW Active site; active domain; growth hormone; somatogenic receptor;  
KW mutagenesis.

XX

OS Synthetic.

XX

PN US5580723-A.

XX

PD 03-DEC-1996.

XX

PF 02-FEB-1994; 94US-00190723.

XX

PR 28-OCT-1988; 88US-00264611.

PR 26-OCT-1989; 89US-00428066.

PR 27-APR-1992; 92US-00875204.

PR 13-OCT-1992; 92US-00960227.

XX

PA (GETH ) GENENTECH INC.  
 XX  
 PI Cunningham BC, Wells JA;  
 XX  
 DR WPI; 1997-033563/03.  
 XX  
 PT Identification of unknown active domains in polypeptide(s) - useful for  
 PT analysis of structure and function of hormones, etc.  
 XX  
 PS Disclosure; Col 26; 86pp; English.  
 XX  
 CC Substitution peptides (AAW10441-62) were used to identify specific amino  
 CC acid residues in human growth hormone (hGH) (AAW10425) which are expected  
 CC to product hGH variants having altered biological functions. The method  
 CC involved substituting selected amino acid segments of hGH with analogous  
 CC segments from analogue polypeptides (human placenta lactogen, human  
 CC prolactin and pig growth hormone) and examining the effect of the  
 CC substns. on interaction with the soluble hGH receptor (see also  
 CC AAW10426). Once active site domains had been detd., amino acid residues  
 CC within these domains were replaced sequentially with alanine, and the  
 CC effects on interaction with the hGH receptor were again examined. Asn-99  
 CC was identified by this method; the preferred amino acid substn. for this  
 CC residue is given in AAW10451. Active site residues have also been  
 CC identified (see also AAW10427-40). (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARQ 3  
 |||  
 Db 5 ARQ 7

# RESULT 57

AAW10433

ID AAW10433 standard; peptide; 11 AA.

XX

AC AAW10433;

XX

DT 25-MAR-2003 (revised)

DT 11-AUG-1997 (first entry)

XX

DE Human growth hormone active site Asp-171 substitution peptide.

XX

KW Active site; active domain; growth hormone; somatogenic receptor;  
 KW mutagenesis.

XX

OS Synthetic.

XX

PN US5580723-A.

XX

PD 03-DEC-1996.

XX

PF 02-FEB-1994; 94US-00190723.  
XX  
PR 28-OCT-1988; 88US-00264611.  
PR 26-OCT-1989; 89US-00428066.  
PR 27-APR-1992; 92US-00875204.  
PR 13-OCT-1992; 92US-00960227.

XX  
PA (GETH ) GENENTECH INC.

XX  
PI Cunningham BC, Wells JA;

XX  
DR WPI; 1997-033563/03.

XX  
PT Identification of unknown active domains in polypeptide(s) - useful for  
PT analysis of structure and function of hormones, etc.

XX  
PS Disclosure; Col 24; 86pp; English.

XX  
CC Substitution peptides (AAW10427-40) were used to identify active site  
CC amino acids within active domains of human growth hormone (hGH)  
CC (AAW10425). The method involved substituting selected amino acid segments  
CC of hGH with analogous segments from analogue polypeptides (human placenta  
CC lactogen, human prolactin and pig growth hormone) and examining the  
CC effect of the substns. on interaction with the soluble hGH receptor (see  
CC also AAW10426). Once active site domains had been detd., amino acid  
CC residues within these domains were replaced sequentially with alanine,  
CC and the effects on interaction with the hGH receptor were again examined.  
CC Asp-171 was identified as an active site residue by this method; the  
CC preferred amino acid substn. for this residue is given in AAW10433.  
CC (Updated on 25-MAR-2003 to correct PF field.)

XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 5 ARQ 7

#### RESULT 58

AAW10459

ID AAW10459 standard; peptide; 11 AA.

XX

AC AAW10459;

XX

DT 25-MAR-2003 (revised)

DT 11-AUG-1997 (first entry)

XX

DE Human growth hormone Asp-26 substitution peptide.

XX

KW Active site; active domain; growth hormone; somatogenic receptor;  
KW mutagenesis.

XX

OS Synthetic.

XX  
 PN US5580723-A.  
 XX  
 PD 03-DEC-1996.  
 XX  
 PF 02-FEB-1994; 94US-00190723.  
 XX  
 PR 28-OCT-1988; 88US-00264611.  
 PR 26-OCT-1989; 89US-00428066.  
 PR 27-APR-1992; 92US-00875204.  
 PR 13-OCT-1992; 92US-00960227.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Cunningham BC, Wells JA;  
 XX  
 DR WPI; 1997-033563/03.  
 XX  
 PT Identification of unknown active domains in polypeptide(s) - useful for  
 PT analysis of structure and function of hormones, etc.  
 XX  
 PS Disclosure; Col 26; 86pp; English.  
 XX  
 CC Substitution peptides (AAW10441-62) were used to identify specific amino  
 CC acid residues in human growth hormone (hGH) (AAW10425) which are expected  
 CC to product hGH variants having altered biological functions. The method  
 CC involved substituting selected amino acid segments of hGH with analogous  
 CC segments from analogue polypeptides (human placenta lactogen, human  
 CC prolactin and pig growth hormone) and examining the effect of the  
 CC substns. on interaction with the soluble hGH receptor (see also  
 CC AAW10426). Once active site domains had been detd., amino acid residues  
 CC within these domains were replaced sequentially with alanine, and the  
 CC effects on interaction with the hGH receptor were again examined. Asp-26  
 CC was identified by this method; the preferred amino acid substn. for this  
 CC residue is given in AAW10459. Active site residues have also been  
 CC identified (see also AAW10427-40). (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
 |||  
 Db 5 ARQ 7

# RESULT 59

AAW10441

ID AAW10441 standard; peptide; 11 AA.

XX

AC AAW10441;

XX

DT 25-MAR-2003 (revised)

DT 11-AUG-1997 (first entry)

XX  
 DE Human growth hormone Ser-43 substitution peptide.  
 XX  
 KW Active site; active domain; growth hormone; somatogenic receptor;  
 KW mutagenesis.  
 XX  
 OS Synthetic.  
 XX  
 PN US5580723-A.  
 XX  
 PD 03-DEC-1996.  
 XX  
 PF 02-FEB-1994; 94US-00190723.  
 XX  
 PR 28-OCT-1988; 88US-00264611.  
 PR 26-OCT-1989; 89US-00428066.  
 PR 27-APR-1992; 92US-00875204.  
 PR 13-OCT-1992; 92US-00960227.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Cunningham BC, Wells JA;  
 XX  
 DR WPI; 1997-033563/03.  
 XX  
 PT Identification of unknown active domains in polypeptide(s) - useful for  
 PT analysis of structure and function of hormones, etc.  
 XX  
 PS Disclosure; Col 26; 86pp; English.  
 XX  
 CC Substitution peptides (AAW10441-62) were used to identify specific amino  
 CC acid residues in human growth hormone (hGH) (AAW10425) which are expected  
 CC to product hGH variants having altered biological functions. The method  
 CC involved substituting selected amino acid segments of hGH with analogous  
 CC segments from analogue polypeptides (human placenta lactogen, human  
 CC prolactin and pig growth hormone) and examining the effect of the  
 CC substns. on interaction with the soluble hGH receptor (see also  
 CC AAW10426). Once active site domains had been detd., amino acid residues  
 CC within these domains were replaced sequentially with alanine, and the  
 CC effects on interaction with the hGH receptor were again examined. Ser-43  
 CC was identified by this method; the preferred amino acid substn. for this  
 CC residue is given in AAW10441. Active site residues have also been  
 CC identified (see also AAW10427-40). (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
 |||  
 Db 5 ARQ 7

RESULT 60

AAW10453  
 ID AAW10453 standard; peptide; 11 AA.  
 XX  
 AC AAW10453;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 11-AUG-1997 (first entry)  
 XX  
 DE Human growth hormone Leu-101 substitution peptide.  
 XX  
 KW Active site; active domain; growth hormone; somatogenic receptor;  
 KW mutagenesis.  
 XX  
 OS Synthetic.  
 XX  
 PN US5580723-A.  
 XX  
 PD 03-DEC-1996.  
 XX  
 PF 02-FEB-1994; 94US-00190723.  
 XX  
 PR 28-OCT-1988; 88US-00264611.  
 PR 26-OCT-1989; 89US-00428066.  
 PR 27-APR-1992; 92US-00875204.  
 PR 13-OCT-1992; 92US-00960227.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Cunningham BC, Wells JA;  
 XX  
 DR WPI; 1997-033563/03.  
 XX  
 PT Identification of unknown active domains in polypeptide(s) - useful for  
 PT analysis of structure and function of hormones, etc.  
 XX  
 PS Disclosure; Col 26; 86pp; English.  
 XX  
 CC Substitution peptides (AAW10441-62) were used to identify specific amino  
 CC acid residues in human growth hormone (hGH) (AAW10425) which are expected  
 CC to product hGH variants having altered biological functions. The method  
 CC involved substituting selected amino acid segments of hGH with analogous  
 CC segments from analogue polypeptides (human placenta lactogen, human  
 CC prolactin and pig growth hormone) and examining the effect of the  
 CC substns. on interaction with the soluble hGH receptor (see also  
 CC AAW10426). Once active site domains had been detd., amino acid residues  
 CC within these domains were replaced sequentially with alanine, and the  
 CC effects on interaction with the hGH receptor were again examined. Leu-101  
 CC was identified by this method; the preferred amino acid substn. for this  
 CC residue is given in AAW10453. Active site residues have also been  
 CC identified (see also AAW10427-40). (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARQ 3  
|||  
Db 5 ARQ 7

RESULT 61

AAW25322

ID AAW25322 standard; peptide; 11 AA.

XX

AC AAW25322;

XX

DT 14-OCT-1997 (first entry)

XX

DE Peptide clone LacI-19 specific for monoclonal antibody D32.39.

XX

KW Monoclonal antibody D32.39; lacI; headpiece domain; DNA binding protein;  
KW random peptide library; receptor ligand; dimer; fusion protein; epitope;  
KW antibody.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Region 6. .11

FT /note= "partial D32.39 antibody epitope"

XX

PN WO9640987-A1.

XX

PD 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US009809.

XX

PR 07-JUN-1995; 95US-00484090.

PR 26-OCT-1995; 95US-00548540.

XX

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX

PI Schatz PJ, Cull MG, Miller JF, Stemmer WPC, Gates CM;

XX

DR WPI; 1997-087065/08.

XX

PT Random peptide library and affinity enrichment methods for screening it -  
PT useful to identify peptide(s) that bind receptors, useful for  
PT therapeutic, diagnostic and related purposes.

XX

PS Example 5; Fig 8; 149pp; English.

XX

CC AAW25289-W25324 represent D32.39 monoclonal antibody specific peptides.  
CC These sequences were isolated by a method of the invention to isolate a  
CC DNA binding protein, or a peptide with specific affinity for a receptor.  
CC The method comprises providing a recombinant DNA vector encoding a  
CC peptide having specific affinity for a receptor. A library of  
CC oligonucleotides encoding different potential DNA binding proteins is  
CC inserted in-frame into the vector to create a fusion protein library.  
CC Host cells are transformed, and cultured to express the fusion protein.  
CC If a fusion protein comprises a potential DNA binding protein with  
CC affinity for the vector, the fusion protein binds to the vector to form a

CC complex. The host cells are lysed to isolate the complexes which are  
CC contacted with a receptor to induce peptide binding to the receptor. The  
CC random peptide library and the methods for screening it can be used to  
CC identify peptides that bind receptor molecules of interest. The peptides  
CC can be used for therapeutic, diagnostic and related purposes, e.g. to  
CC bind the receptor, or an analogue, and so inhibit or promote the activity  
CC of the receptor. The method of affinity enrichment allows a very large  
CC library of peptides to be screened, and by identifying the peptide de  
CC novo, the sequence or structure of the receptor molecule or the natural  
CC binding partner of the receptor need not be known

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11

|||

Db 5 RRS 7

#### RESULT 62

AAW25307

ID AAW25307 standard; peptide; 11 AA.

XX

AC AAW25307;

XX

DT 14-OCT-1997 (first entry)

XX

DE Peptide clone LacI-1 specific for monoclonal antibody D32.39.

XX

KW Monoclonal antibody D32.39; lacI; headpiece domain; DNA binding protein;

KW random peptide library; receptor ligand; dimer; fusion protein; epitope;

KW antibody.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Region 6. .11

FT /note= "partial D32.39 antibody epitope"

XX

PN W09640987-A1.

XX

PD 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US009809.

XX

PR 07-JUN-1995; 95US-00484090.

PR 26-OCT-1995; 95US-00548540.

XX

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX

PI Schatz PJ, Cull MG, Miller JF, Stemmer WPC, Gates CM;

XX

DR WPI; 1997-087065/08.

XX



PT Random peptide library and affinity enrichment methods for screening it -  
PT useful to identify peptide(s) that bind receptors, useful for  
PT therapeutic, diagnostic and related purposes.

XX

PS Example 5; Fig 8; 149pp; English.

XX

CC AAW25289-W25324 represent D32.39 monoclonal antibody specific peptides.  
CC These sequences were isolated by a method of the invention to isolate a  
CC DNA binding protein, or a peptide with specific affinity for a receptor.  
CC The method comprises providing a recombinant DNA vector encoding a  
CC peptide having specific affinity for a receptor. A library of  
CC oligonucleotides encoding different potential DNA binding proteins is  
CC inserted in-frame into the vector to create a fusion protein library.  
CC Host cells are transformed, and cultured to express the fusion protein.  
CC If a fusion protein comprises a potential DNA binding protein with  
CC affinity for the vector, the fusion protein binds to the vector to form a  
CC complex. The host cells are lysed to isolate the complexes which are  
CC contacted with a receptor to induce peptide binding to the receptor. The  
CC random peptide library and the methods for screening it can be used to  
CC identify peptides that bind receptor molecules of interest. The peptides  
CC can be used for therapeutic, diagnostic and related purposes, e.g. to  
CC bind the receptor, or an analogue, and so inhibit or promote the activity  
CC of the receptor. The method of affinity enrichment allows a very large  
CC library of peptides to be screened, and by identifying the peptide de  
CC novo, the sequence or structure of the receptor molecule or the natural  
CC binding partner of the receptor need not be known

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 5 RRS 7

#### RESULT 63

AAW09807

ID AAW09807 standard; peptide; 11 AA.

XX

AC AAW09807;

XX

DT 25-MAR-2003 (revised)

DT 12-JUN-1997 (first entry)

XX

DE N-terminal peptide fragment of erythrocyte cytoplasmic PAF-AH.

XX

KW Human platelet-activating factor acetylhydrolase; PAF-AH; detection;  
KW mutation; V279F; substitution; restriction fragment length polymorphism;  
KW analysis; diagnosis; inherited; deficiency; severe respiratory symptom;  
KW asthmatic children; treat; inflammatory condition.

XX

OS Synthetic.

XX

PN US5605801-A.

XX  
PD 25-FEB-1997.  
XX  
PF 07-JUN-1995; 95US-00478465.  
XX  
PR 06-OCT-1993; 93US-00133803.  
PR 06-OCT-1994; 94US-00318905.  
XX  
PA (ICOS-) ICOS CORP.  
XX  
PI Gray P, Tjoelker LW, Trong HL, Cousens LS, Wilder CL;  
PI Eberhardt CD;  
XX  
DR WPI; 1997-153573/14.  
XX  
PT Detection of platelet-activating factor acetylhydrolase gene mutation -  
PT by restriction length polymorphism analysis.  
XX  
PS Example 2; Col 11; 43pp; English.  
XX  
CC An approx. 44 kDa protein band from a human platelet-activating factor  
CC acetylhydrolase (PAF-AH)-containing PVDF membrane was excised and  
CC sequenced. N-terminal sequence analysis of the 44 kDa protein band  
CC corresponding to the PAF-AH activity indicated that the band contained  
CC two major and two minor sequences. The ratio of the two major sequences  
CC was 1:1 and it was therefore difficult to interpret the data. To  
CC distinguish the sequences of the two major proteins which had been  
CC resolved on the SDS gel, a duplicate PVDF membrane contg. the 44 kDa band  
CC was cut in half such that the upper and lower part of the membrane were  
CC separately subjected to sequencing. AAW09805-06 are the N-terminal  
CC peptide sequences obtained. It was revealed that AAW09806 was the novel  
CC sequence representing the N-terminal peptide of human PAF-AH. It was  
CC compared against the present sequence which is the N-terminal sequence of  
CC erythrocyte cytoplasmic PAF-AH. The claimed method of the invention  
CC detects a mutation (which results in a V279F substitution) in the PAF-AH  
CC gene, and comprises performing a restriction fragment length polymorphism  
CC analysis and differentiating between wild-type and mutant alleles on the  
CC basis of the number of restriction sites. The method is useful for  
CC diagnosis of inherited PAF-AH deficiency, which has been correlated with  
CC severe respiratory symptoms in asthmatic children. Recombinant PAF-AH can  
CC be used to treat inflammatory conditions. (Updated on 25-MAR-2003 to  
CC correct PF field.)  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 1 MKP 3

RESULT 64  
AAW11150  
ID AAW11150 standard; peptide; 11 AA.

XX  
 AC AAW11150;  
 XX  
 DT 10-JUN-1997 (first entry)  
 XX  
 DE CD4 peptide capable of binding HIV gp120 to inactivate HIV.  
 XX  
 KW HIV; human immunodeficiency virus; gp120; glycoprotein 120; AIDS;  
 KW acquired immune deficiency syndrome; inhibit transmission.  
 XX  
 OS Synthetic.  
 XX  
 PN US5603933-A.  
 XX  
 PD 18-FEB-1997.  
 XX  
 PF 31-AUG-1993; 93US-00115171.  
 XX  
 PR 31-AUG-1993; 93US-00115171.  
 XX  
 PA (TEXA ) UNIV TEXAS.  
 XX  
 PI Sastry JK, Dwyer VA, Arlinghaus RB, Nehete PN;  
 XX  
 DR WPI; 1997-144820/13.  
 XX  
 PT Compsn. comprising CD4 peptide capable of binding to HIV gp120 - for  
 PT protection against HIV infection.  
 XX  
 PS Claim 7; Col 30; 20pp; English.  
 XX  
 CC AAW11147-W11150 are CD4 peptides that bind to HIV gp120 and inactivate  
 CC the virus. The peptides can be dispersed in a suitable vehicle to provide  
 CC compositions useful for protecting human CD4+ cells, e.g. T cells, from  
 CC HIV infection, e.g. to inhibit transmission of HIV during sexual contact.  
 CC They could also be used in e.g. surgical gloves and liquid soap in  
 CC hospitals to prevent HIV transmission. Alternatively, the peptides in the  
 CC composition may be attached to solid supports, e.g. disposable filters,  
 CC for inactivating HIV in blood and other body fluid samples  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11  
 |||  
 Db 8 RRS 10

RESULT 65  
 AAW39790  
 ID AAW39790 standard; protein; 11 AA.  
 XX  
 AC AAW39790;  
 XX

DT 11-JUN-1998 (first entry)  
 XX  
 DE Mammalian HMG-Yc repeated AT hook.  
 XX  
 KW Palindromic element binding factor; PABF; tobacco; cis-acting element;  
 KW transcription enhancer; heterologous promoter; AATT repeat element;  
 KW transcription factor; AT hook; HMG I/Y protein.  
 XX  
 OS Mammalia.  
 XX  
 PN WO9749727-A1.  
 XX  
 PD 31-DEC-1997.  
 XX  
 PF 27-JUN-1997; 97WO-US011156.  
 XX  
 PR 27-JUN-1996; 96US-00669721.  
 XX  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 XX  
 PI Lamb CJ, Doerner P, Laible G;  
 XX  
 DR WPI; 1998-077110/07.  
 XX  
 PT New isolated enhancer and transcription factor - used for increasing the  
 PT recombinant expression of proteins, particularly in plants, e.g. for  
 PT increasing production or providing pest resistance.  
 XX  
 PS Disclosure; Fig 7B; 65pp; English.  
 XX  
 CC AAW39790-W39796 are AT hook motifs used in the characterisation of a  
 CC novel tobacco palindromic element binding factor, (PABF). This PABF binds  
 CC to the sequence (AATT)<sub>n</sub> where n at least 2. The (AATT)<sub>n</sub> sequence has cis-  
 CC acting, non-specific enhancer activity. It can be linked to a  
 CC heterologous promoter operably linked with a gene to increase expression  
 CC of the gene in a cell, particularly in plants. It can provide for  
 CC increased expression of proteins such as nutritionally important  
 CC proteins, growth promoting factors, proteins for early flowering in  
 CC plants, proteins giving protection to the plant under certain  
 CC environmental conditions, e.g. proteins conferring resistance to metals  
 CC or other toxic substances, such as herbicides or pesticides, stress-  
 CC related proteins which confer tolerance to temperature extremes, proteins  
 CC conferring resistance to fungi, bacteria, viruses, insects and nematodes,  
 CC proteins of specific commercial value, e.g. enzymes involved in metabolic  
 CC pathways, such as EPSP synthase. The PABF polypeptides act as  
 CC transcription factor and bind to the (AATT) repeat element to further  
 CC boost the activity of the enhancer  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9  
 |||  
 Db 4 KPR 6

RESULT 66

AAW66283

ID AAW66283 standard; peptide; 11 AA.

XX

AC AAW66283;

XX

DT 23-NOV-1998 (first entry)

XX

DE SMR1 peptide useful in treating mineral imbalance associated diseases.

XX

KW mineral ion imbalance; submandibular rat protein 1; SMR1; osteoporosis;

KW pancreatitis; nephrolithiasis.

XX

OS Synthetic.

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Misc-difference 1. .11

FT /note= "Optionally one or more amino acids are in the D-  
FT form"

XX

PN WO9837100-A2.

XX

PD 27-AUG-1998.

XX

PF 19-FEB-1998; 98WO-EP000956.

XX

PR 20-FEB-1997; 97US-00801405.

XX

PA (INSP ) INST PASTEUR.

XX

PI Rougeot C, Rougeon F;

XX

DR WPI; 1998-480790/41.

XX

PT Treating disease associated with mineral imbalance using submandibular

PT rat 1 protein - or its derivatives, e.g. osteoporosis, pancreatitis,

PT nephrolithiasis etc., also related ligands and receptor complexes.

XX

PS Claim 3 and 4; Page 79; 111pp; English.

XX

CC The invention relates to a method for treating or preventing diseases  
CC caused by a mineral ion imbalance. The method comprises administration of  
CC submandibular rat (SMR)1 protein, its maturation products and  
CC biologically active derivatives. These therapeutic compounds are used to  
CC control mineral imbalances in kidney, bone, dental enamel or ivory,  
CC intestine, pancreas, glandular gastric mucosa and parathyroid, e.g. hyper  
CC - or hypo-parathyroidism, osteoporosis, pancreatitis, submandibular gland  
CC lithiasis, nephrolithiasis and osteodystrophy. The present sequence  
CC represents a preferred SMR1 maturation product which can be used in the  
CC method

XX

SQ Sequence 11 AA;

Query Match

27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 4 PRR 6

RESULT 67

AAW53849

ID AAW53849 standard; peptide; 11 AA.

XX

AC AAW53849;

XX

DT 09-JUL-1998 (first entry)

XX

DE Protein kinase substrate, peptide 2.

XX

KW Protein kinase substrate; kinase activity detection.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal Biotin"

XX

PN WO9809169-A1.

XX

PD 05-MAR-1998.

XX

PF 26-AUG-1997; 97WO-US015023.

XX

PR 26-AUG-1996; 96US-00702970.

XX

PA (TULA-) TULARIK INC.

XX

PI Strulovici B;

XX

DR WPI; 1998-179583/16.

XX

PT Determining kinase activity without radioactive reagents - by using  
PT kinase to introduce phosphorylation-dependent tag into substrate and  
PT detecting this with receptor, after immobilisation through a separate  
PT tag.

XX

PS Disclosure; Page 8; 28pp; English.

XX

CC This sequence represents a protein kinase substrate used in the method of  
CC the invention. The method is for determining kinase activity, and  
CC comprises: (i) incubating a solution containing kinase, first receptor  
CC (R1), nucleotide triphosphate (NTP) and kinase substrate containing a  
CC first phosphorylation-independent tag and acquiring a second  
CC phosphorylation-dependent tag during incubation; (ii) incubating so that  
CC R1 immobilises the product on a solid support by binding specifically to  
CC one tag; (iii) washing the support; (iv) treating the immobilised product  
CC with a second receptor (R2) that binds specifically to the unreacted tag;  
CC and (v) washing again and detecting R2 to indicate presence of

CC phosphorylation and thus of kinase activity. The method can be used to  
CC detect kinase activity as such, or to screen compounds for modulation of  
CC kinase activity. Kinase activity is determined without use of  
CC radioactivity and all reagents used are storage stable. The method  
CC combines rapidity of solution phase reactions and the efficiency and  
CC adaptability to high throughput screening of solid phase processes. Assay  
CC is fast (2-3 hours), simple to do (all steps in a single vessel) and very  
CC sensitive. Also it produces a signal that correlates with ATP (adenosine  
CC triphosphate) concentration, allowing assays to be performed at high,  
CC nearly physiological, ATP levels

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11

|||

Db 9 RRS 11

#### RESULT 68

AAW38368

ID AAW38368 standard; protein; 11 AA.

XX

AC AAW38368;

XX

DT 31-MAR-1998 (first entry)

XX

DE Human plasma PAF-AH amino-terminal fragment.

XX

KW Human; plasma platelet activating factor acetylhydrolase;

KW monoclonal antibody; immunoassay; diagnosis; asthma; PAF-AH; detection;

KW amino-terminal.

XX

OS Homo sapiens.

XX

PN US5698403-A.

XX

PD 16-DEC-1997.

XX

PF 07-JUN-1995; 95US-00483140.

XX

PR 06-OCT-1993; 93US-00133803.

PR 06-OCT-1994; 94US-00318905.

XX

PA (ICOS-) ICOS CORP.

XX

PI Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;

PI Eberhardt CD;

XX

DR WPI; 1998-051484/05.

XX

PT Immunoassay for platelet activating factor acetylhydrolase, PAF-AH -

PT useful to diagnose disorders associated with abnormal PAF-AH level.

XX

PS Example 2; Col 33-34; 47pp; English.

XX

CC The present sequence was used in the development of a method for  
CC detecting human, mouse, canine, rat and monkey plasma platelet activating  
CC factor acetylhydrolases (PAF-AH). The method comprises contacting serum  
CC with PAF-AH specific monoclonal antibody (MAb) to form a PAF-AH/MAb  
CC complex, and detecting the complex. The method can be used to diagnose  
CC disorders associated with abnormal PAF-AH levels, and to monitor therapy  
CC of such disorders. Plasma PAF-AH deficiency has been correlated with  
CC severe respiratory symptoms in asthmatic children who appear to have  
CC inherited the deficiency in an autosomal recessive manner

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8

|||

Db 1 MKP 3

#### RESULT 69

AAY30260

ID AAY30260 standard; peptide; 11 AA.

XX

AC AAY30260;

XX

DT 23-NOV-1999 (first entry)

XX

DE KDR/Flk-1 targeting peptide RP824.

XX

KW Angiogenesis; tumour; metastasis; wound healing; diabetic retinopathy;

KW rheumatoid arthritis; psoriasis; cancer; KDR; kinase domain receptor;

KW vascular endothelial growth factor receptor; VEGF; Flk-1; blood supply;

KW imaging; treatment.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 5

FT /note= "Lys optionally has the sequence DmGSCG or DmGCSG  
FT attached to the side chain, where DmG = Dimethylglycine;  
FT Lys is a D form residue"

XX

PN WO9940947-A2.

XX

PD 19-AUG-1999.

XX

PF 11-FEB-1999; 99WO-CA000101.

XX

PR 11-FEB-1998; 98US-0074420P.

XX

PA (RESO-) RESOLUTION PHARM INC.

XX

PI Fauconnier T, Pollak A, Thornback J, Eshima D;



XX  
 DR WPI; 1999-527342/44.  
 XX  
 PT Angiogenesis targeting molecules, for, e.g. detecting and treating  
 PT cancer.  
 XX  
 PS Example 2; Page 33; 70pp; English.  
 XX  
 CC Sequences AAY30241-Y30273 are peptides that target the Kinase Domain  
 CC Receptor (KDR) murine homologue Flk-1. KDR is a high affinity receptor  
 CC for vascular endothelial growth factor (VEGF) found on endothelial cells.  
 CC VEGF has been shown to induce angiogenesis, which is the process involved  
 CC in creating a blood supply to a tumour. The peptides are used in a  
 CC compound that binds to sites of angiogenesis. The compound consists of a  
 CC chelator moiety capable of complexing a radionuclide metal or a moiety  
 CC capable of binding to a halogen group, and an angiogenesis targeting  
 CC molecule. The peptides are incorporated in the angiogenesis targeting  
 CC molecule. The compounds are used for imaging and treating angiogenesis,  
 CC and also to detect, stage and treat tumours and metastases. Angiogenesis  
 CC is also required for wound healing and conditions such as diabetic  
 CC retinopathy, rheumatoid arthritis and psoriasis, therefore the compounds  
 CC may also be useful in the treatment of these conditions  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
 |||  
 Db 5 KPR 7

# RESULT 70

AAY30265

ID AAY30265 standard; peptide; 11 AA.

XX

AC AAY30265;

XX

DT 23-NOV-1999 (first entry)

XX

DE KDR/Flk-1 targeting peptide RP849.

XX

KW Angiogenesis; tumour; metastasis; wound healing; diabetic retinopathy;  
 KW rheumatoid arthritis; psoriasis; cancer; KDR; kinase domain receptor;  
 KW vascular endothelial growth factor receptor; VEGF; Flk-1; blood supply;  
 KW imaging; treatment.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Beta alanine"

FT Modified-site 2

FT /note= "Lys has the sequence IYEI attached to the side  
 FT chain"

XX  
 PN WO9940947-A2.  
 XX  
 PD 19-AUG-1999.  
 XX  
 PF 11-FEB-1999; 99WO-CA000101.  
 XX  
 PR 11-FEB-1998; 98US-0074420P.  
 XX  
 PA (RESO-) RESOLUTION PHARM INC.  
 XX  
 PI Fauconnier T, Pollak A, Thornback J, Eshima D;  
 XX  
 DR WPI; 1999-527342/44.  
 XX  
 PT Angiogenesis targeting molecules, for, e.g. detecting and treating  
 PT cancer.  
 XX  
 PS Example 2; Page 33; 70pp; English.  
 XX  
 CC Sequences AAY30241-Y30273 are peptides that target the Kinase Domain  
 CC Receptor (KDR) murine homologue Flk-1. KDR is a high affinity receptor  
 CC for vascular endothelial growth factor (VEGF) found on endothelial cells.  
 CC VEGF has been shown to induce angiogenesis, which is the process involved  
 CC in creating a blood supply to a tumour. The peptides are used in a  
 CC compound that binds to sites of angiogenesis. The compound consists of a  
 CC chelator moiety capable of complexing a radionuclide metal or a moiety  
 CC capable of binding to a halogen group, and an angiogenesis targeting  
 CC molecule. The peptides are incorporated in the angiogenesis targeting  
 CC molecule. The compounds are used for imaging and treating angiogenesis,  
 CC and also to detect, stage and treat tumours and metastases. Angiogenesis  
 CC is also required for wound healing and conditions such as diabetic  
 CC retinopathy, rheumatoid arthritis and psoriasis, therefore the compounds  
 CC may also be useful in the treatment of these conditions  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
 |||  
 Db 2 KPR 4

# RESULT 71

AAW96333

ID AAW96333 standard; peptide; 11 AA.

XX

AC AAW96333;

XX

DT 28-JUN-1999 (first entry)

XX

DE Human erythrocyte cytoplasmic PAF-AH N-terminal peptide.

XX

KW Plasma platelet activating factor acetylhydrolase; PAF-AH; PAF;

KW platelet activating factor; inflammation; treatment; hydrolysis;  
 KW augmentation; pleurisy; asthma; rhinitis; necrotizing enterocolitis;  
 KW acute respiratory distress syndrome; pancreatitis; PCR primer;  
 KW neurological disease; HIV; human immunodeficiency virus.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9909147-A1.  
 XX  
 PD 25-FEB-1999.  
 XX  
 PF 13-AUG-1997; 97WO-US014212.  
 XX  
 PR 13-AUG-1997; 97WO-US014212.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;  
 PI Wilder CL;  
 XX  
 DR WPI; 1999-181028/15.  
 XX  
 PT New truncated human platelet-activating factor acetylhydrolase and its  
 PT encoding polynucleotides - useful for regulating inflammatory events.  
 XX  
 PS Example 2; Page 23; 136pp; English.  
 XX  
 CC When trying to isolate the human plasma platelet-activating factor  
 CC acetylhydrolase (PAF-AH) sequence, two candidate protein sequences for  
 CC PAF-AH were isolated, both of 44kDA. N-terminal analyses of these  
 CC proteins showed that one of them was human serum albumin. The other N-  
 CC terminal peptide (AAW96332) was was not matched on any databases  
 CC searched. It differed from the N-terminal sequence of erythrocyte  
 CC cytoplasmic PAF-AH and was thus used to generate a degenerate primer  
 CC (AAX08485) used to screen a macrophage library for the plasma PAF-AH  
 CC sequence. PAF-AH can be used to inactivate the pathological effects of  
 CC PAF. Pathological conditions which can be treated include pleurisy,  
 CC asthma, rhinitis, necrotizing enterocolitis, acute respiratory distress  
 CC syndrome, acute pancreatitis or neurological disease associated with HIV  
 CC infection. Identification and isolation of polynucleotide sequences  
 CC encoding human plasma PAF-AH allows the recombinant production of PAF-AH.  
 CC This makes possible the use of exogenous PAF-AH to mimic or augment  
 CC normal processes of resolution of inflammation in vivo. PAF inactivation  
 CC occurs by hydrolysis of the PAF sn-2 acetyl group by PAF-AH. PAF-AH also  
 CC metabolises oxidatively fragmented phospholipids such as products of the  
 CC arachidonic acid cascade which mediate inflammation. Administration of  
 CC PAF-AH is advantageous to administering PAF receptor antagonists since  
 CC PAF-AH is a product normally found in plasma. Because PAF receptor  
 CC antagonists are structurally related to PAF they competitively inhibit  
 CC native PAF-AH activity. Treatment with recombinant PAF-AH would augment  
 CC endogenous PAF-AH activity and compensate for any inactivated  
 CC endogenous enzyme  
 XX  
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 1 MKP 3

RESULT 72

AAY30081

ID AAY30081 standard; peptide; 11 AA.

XX

AC AAY30081;

XX

DT 11-OCT-1999 (first entry)

XX

DE A complement activity inhibiting peptide.

XX

KW Complement activity; complement component C1; activation; inhibition;  
KW hemolysis; multiple peptide antigen.

XX

OS Synthetic.

XX

PN JP11199599-A.

XX

PD 27-JUL-1999.

XX

PF 09-DEC-1997; 97JP-00338964.

XX

PR 09-DEC-1997; 97JP-00338964.

XX

PA (DCAR/) DEL CARPIO C A.

PA (KOJI/) KOJIMA H.

PA (KOB/) KOBAYASHI M.

PA (AZUM/) AZUMA N.

XX

DR WPI; 1999-474074/40.

XX

PT A complement activity inhibiting peptide and an anti-complementary agent  
PT - useful for inhibiting e.g. hemolysis.

XX

PS Claim 1; Page 2; 8pp; Japanese.

XX

CC The present sequence represents a a complement activity inhibiting  
CC peptide. The peptide can be used to make a diploid (two units connected  
CC to each other through free Lys), a tetraploid (two diploids), an octaploid  
CC (two tetraploids) and a hexadecaploid (two octaploids). The peptide combines  
CC to the complement component C1 to inhibit its activation. The peptide is  
CC used, for example, for inhibiting hemolysis

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||

## RESULT 73

AAY45419

ID AAY45419 standard; peptide; 11 AA.

XX

AC AAY45419;

XX

DT 01-DEC-1999 (first entry)

XX

DE Immunogenic peptide having a human leukocyte antigen binding motif #30.

XX

KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;

KW immune response; T cell activation; major histocompatibility complex;

KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;

KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;

KW vaccine; immunisation.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9945954-A1.

XX

PD 16-SEP-1999.

XX

PF 13-MAR-1998; 98WO-US005039.

XX

PR 13-MAR-1998; 98WO-US005039.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX

DR WPI; 1999-551214/46.

XX

PT New immunogenic peptides with HLA binding motif, useful in treatment and

PT diagnosis of cancers and viral diseases.

XX

PS Claim 1; Page 28; 150pp; English.

XX

CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
CC having a human major histocompatibility complex (MHC) Class I (also known  
CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides  
CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2  
CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against  
CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes  
CC (CTLs) which destroy antigen-bearing cells are normally induced by an  
CC antigen in the form of a peptide fragment bound to a HLA molecule, rather  
CC than the intact foreign antigen itself, and are particularly important in  
CC tumour rejection and in fighting viral infections. The peptides are  
CC therefore useful therapeutically to treat or prevent viral infections and  
CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B  
CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to  
CC elicit an immune response in individuals susceptible or otherwise at risk  
CC of viral infection or cancer, or used to treat chronic or acute  
CC conditions. They are also useful diagnostically, and can be used to

CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with  
CC the peptide e.g. to produce CTLs ex vivo for infusion back into a  
CC patient. The polynucleotides encoding the immunogenic peptides are also  
CC useful therapeutically and for immunisation as above  
XX  
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 5 PRR 7

RESULT 74

AAY42687

ID AAY42687 standard; peptide; 11 AA.

XX

AC AAY42687;

XX

DT 17-JAN-2000 (first entry)

XX

DE HHV-6 variant B derived peptide epitope.

XX

KW Human herpes virus-6; HHV-6; infection; immunological; MIEP; epitope;  
KW major immediate early protein.

XX

OS Synthetic.

OS Human herpesvirus 6.

XX

PN WO9949086-A1.

XX

PD 30-SEP-1999.

XX

PF 26-MAR-1999; 99WO-US006921.

XX

PR 26-MAR-1998; 98US-0079379P.

PR 23-MAR-1999; 99US-00274938.

XX

PA (CARR/) CARRIGAN D R.

PA (KEHL/) KEHL K K.

XX

PI Carrigan DR, Kehl KK;

XX

DR WPI; 1999-601224/51.

XX

PT Methods for the rapid detection of human herpes virus 6 variants A and B  
PT utilizing antibodies raised against synthetic peptides.

XX

PS Claim 17; Page 42; 58pp; English.

XX

CC The invention relates to a method for detecting human herpes virus (HHV)-  
CC 6 infection that comprises contacting host cells with immunological  
CC reagents specific for an epitope of HHV-6 variant A and/or B major  
CC immediate early protein (MIEP). HHV-6 peptides for raising an

CC immunological reagent that binds specifically to an epitope of: (a) HHV-6  
CC variant A and not B MIEP; or (b) HHV-6 variant A and B MIEP are also  
CC provided. The peptides are useful as immunological reagents, e.g.  
CC hyperimmune sera. Monoclonal antibodies and recombinant DNA-derived  
CC single chain fragment variables (ScFv) may be useful for detecting HHV-6  
CC infection when raised against specific epitopes of the HHV-6 MIEP. The  
CC methods provide a rapid culture procedure having a high level of  
CC sensitivity and specificity. The methods also have shortened turnaround  
CC time (compared to other known methods, e.g. the isolation of the virus in  
CC cell culture, the detection of virus DNA in an acellular specimen by PCR  
CC or positive immunohistochemical staining) and can be easily implemented  
CC by a diagnostic laboratory

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
| | |  
Db 9 KPR 11

#### RESULT 75

AAW73368

ID AAW73368 standard; protein; 11 AA.

XX

AC AAW73368;

XX

DT 12-FEB-1999 (first entry)

XX

DE Human PAF-AH protein fragment.

XX

KW Platelet-activating factor acetylhydrolase; PAF-AH; human; antibody.

XX

OS Homo sapiens.

XX

PN US5847088-A.

XX

PD 08-DEC-1998.

XX

PF 07-JUN-1995; 95US-00485938.

XX

PR 06-OCT-1993; 93US-00133803.

PR 06-OCT-1994; 94US-00318905.

XX

PA (ICOS-) ICOS CORP.

XX

PI Wilder CL, Tjoelker LW, Gray P, Eberhardt CD, Cousens LS;

PI Trong HL;

XX

DR WPI; 1999-059148/05.

XX

PT Antibodies specific for platelet-activating factor acetylhydrolase  
PT proteins - useful for detecting or purifying the proteins.

XX

PS Example 2; Col 12; 59pp; English.

XX

CC This sequence represents a fragment of the human platelet-activating  
CC factor acetylhydrolase (PAF-AH). This protein is specifically bound by  
CC the antibody of the invention. The monoclonal antibody of the invention  
CC is useful for detecting or purifying PAF-AH proteins

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8

|||

Db 1 MKP 3

Search completed: April 8, 2004, 15:39:58

Job time : 46.3077 secs



OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds  
 (without alignments)  
 50.221 Million cell updates/sec

Title: US-09-787-443A-12  
 Perfect score: 11  
 Sequence: 1 ARQKTMKPRRS 11

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11  
 Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
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 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	4	36.4	11	4	US-09-528-200-172	Sequence 172, App
2	3	27.3	11	1	US-07-666-719-18	Sequence 18, Appl
3	3	27.3	11	1	US-07-755-161A-9	Sequence 9, Appli
4	3	27.3	11	1	US-07-891-174-9	Sequence 9, Appli
5	3	27.3	11	1	US-08-046-538-1	Sequence 1, Appli
6	3	27.3	11	1	US-08-197-795-5	Sequence 5, Appli
7	3	27.3	11	1	US-08-128-971B-15	Sequence 15, Appl
8	3	27.3	11	1	US-08-470-187-3	Sequence 3, Appli
9	3	27.3	11	1	US-08-318-905-3	Sequence 3, Appli
10	3	27.3	11	1	US-08-483-232-3	Sequence 3, Appli
11	3	27.3	11	1	US-08-256-771-32	Sequence 32, Appl

12	3	27.3	11	1	US-08-462-917-10	Sequence 10, Appl
13	3	27.3	11	1	US-08-483-140-3	Sequence 3, Appli
14	3	27.3	11	1	US-08-323-531-32	Sequence 32, Appl
15	3	27.3	11	1	US-08-548-540-145	Sequence 145, App
16	3	27.3	11	1	US-08-548-540-160	Sequence 160, App
17	3	27.3	11	1	US-08-198-094-32	Sequence 32, Appl
18	3	27.3	11	1	US-08-702-970-2	Sequence 2, Appli
19	3	27.3	11	1	US-08-381-984-32	Sequence 32, Appl
20	3	27.3	11	2	US-08-669-721-16	Sequence 16, Appl
21	3	27.3	11	2	US-08-485-938A-3	Sequence 3, Appli
22	3	27.3	11	2	US-08-464-182A-11	Sequence 11, Appl
23	3	27.3	11	2	US-08-464-182A-12	Sequence 12, Appl
24	3	27.3	11	2	US-08-693-274A-3	Sequence 3, Appli
25	3	27.3	11	2	US-08-693-274A-4	Sequence 4, Appli
26	3	27.3	11	2	US-08-637-759B-211	Sequence 211, App
27	3	27.3	11	2	US-08-679-865-35	Sequence 35, Appl
28	3	27.3	11	2	US-08-727-688-24	Sequence 24, Appl
29	3	27.3	11	2	US-08-406-271-11	Sequence 11, Appl
30	3	27.3	11	2	US-08-406-271-12	Sequence 12, Appl
31	3	27.3	11	2	US-08-680-876-35	Sequence 35, Appl
32	3	27.3	11	2	US-08-934-222-77	Sequence 77, Appl
33	3	27.3	11	2	US-08-933-402-77	Sequence 77, Appl
34	3	27.3	11	2	US-09-207-621-77	Sequence 77, Appl
35	3	27.3	11	2	US-08-532-818-77	Sequence 77, Appl
36	3	27.3	11	2	US-08-910-041-3	Sequence 3, Appli
37	3	27.3	11	3	US-08-871-355A-211	Sequence 211, App
38	3	27.3	11	3	US-08-159-339A-1139	Sequence 1139, Ap
39	3	27.3	11	3	US-09-328-474-3	Sequence 3, Appli
40	3	27.3	11	3	US-09-231-797-77	Sequence 77, Appl
41	3	27.3	11	3	US-08-609-236-5	Sequence 5, Appli
42	3	27.3	11	3	US-09-100-546-3	Sequence 3, Appli
43	3	27.3	11	3	US-08-934-224-77	Sequence 77, Appl
44	3	27.3	11	3	US-08-933-843-77	Sequence 77, Appl
45	3	27.3	11	3	US-09-010-715-3	Sequence 3, Appli
46	3	27.3	11	3	US-08-934-223-77	Sequence 77, Appl
47	3	27.3	11	3	US-08-836-075A-107	Sequence 107, App
48	3	27.3	11	3	US-08-836-075A-108	Sequence 108, App
49	3	27.3	11	3	US-08-602-999A-290	Sequence 290, App
50	3	27.3	11	3	US-08-652-877-41	Sequence 41, Appl
51	3	27.3	11	3	US-09-189-344-16	Sequence 16, Appl
52	3	27.3	11	3	US-09-577-758-3	Sequence 3, Appli
53	3	27.3	11	3	US-09-208-966-4	Sequence 4, Appli
54	3	27.3	11	3	US-09-208-966-40	Sequence 40, Appl
55	3	27.3	11	3	US-09-208-966-55	Sequence 55, Appl
56	3	27.3	11	3	US-09-208-966-56	Sequence 56, Appl
57	3	27.3	11	3	US-09-208-966-57	Sequence 57, Appl
58	3	27.3	11	3	US-08-107-794A-32	Sequence 32, Appl
59	3	27.3	11	3	US-08-476-515A-41	Sequence 41, Appl
60	3	27.3	11	3	US-09-263-975-35	Sequence 35, Appl
61	3	27.3	11	3	US-09-413-492-77	Sequence 77, Appl
62	3	27.3	11	3	US-09-044-411-7	Sequence 7, Appli
63	3	27.3	11	4	US-09-201-945-211	Sequence 211, App
64	3	27.3	11	4	US-09-227-357-423	Sequence 423, App
65	3	27.3	11	4	US-09-187-859-3080	Sequence 3080, Ap
66	3	27.3	11	4	US-09-187-859-3125	Sequence 3125, Ap
67	3	27.3	11	4	US-09-187-859-3170	Sequence 3170, Ap
68	3	27.3	11	4	US-09-187-859-3215	Sequence 3215, Ap

69	3	27.3	11	4	US-09-187-859-3260	Sequence 3260, Ap
70	3	27.3	11	4	US-09-500-124-290	Sequence 290, App
71	3	27.3	11	4	US-09-347-926-20	Sequence 20, Appl
72	3	27.3	11	4	US-09-588-417-5	Sequence 5, Appli
73	3	27.3	11	4	US-09-839-743-19	Sequence 19, Appl
74	3	27.3	11	4	US-09-260-629-15	Sequence 15, Appl
75	3	27.3	11	4	US-09-129-192C-35	Sequence 35, Appl
76	3	27.3	11	4	US-09-410-551B-35	Sequence 35, Appl
77	3	27.3	11	4	US-09-410-551B-41	Sequence 41, Appl
78	3	27.3	11	4	US-09-410-551B-53	Sequence 53, Appl
79	3	27.3	11	4	US-09-817-310-5	Sequence 5, Appli
80	3	27.3	11	4	US-09-839-542B-3080	Sequence 3080, Ap
81	3	27.3	11	4	US-09-839-542B-3125	Sequence 3125, Ap
82	3	27.3	11	4	US-09-839-542B-3170	Sequence 3170, Ap
83	3	27.3	11	4	US-09-839-542B-3215	Sequence 3215, Ap
84	3	27.3	11	4	US-09-839-542B-3260	Sequence 3260, Ap
85	3	27.3	11	4	US-08-801-405B-6	Sequence 6, Appli
86	3	27.3	11	4	US-09-802-109A-7	Sequence 7, Appli
87	3	27.3	11	4	US-09-630-250B-15	Sequence 15, Appl
88	3	27.3	11	4	US-09-591-694-32	Sequence 32, Appl
89	3	27.3	11	4	US-09-535-852-424	Sequence 424, App
90	3	27.3	11	4	US-09-535-852-469	Sequence 469, App
91	3	27.3	11	4	US-09-535-852-514	Sequence 514, App
92	3	27.3	11	4	US-09-535-852-559	Sequence 559, App
93	3	27.3	11	4	US-09-535-852-604	Sequence 604, App
94	3	27.3	11	4	US-09-535-852-2001	Sequence 2001, Ap
95	3	27.3	11	4	US-09-775-052A-4	Sequence 4, Appli
96	3	27.3	11	4	US-09-775-052A-40	Sequence 40, Appl
97	3	27.3	11	4	US-09-775-052A-55	Sequence 55, Appl
98	3	27.3	11	4	US-09-775-052A-56	Sequence 56, Appl
99	3	27.3	11	4	US-09-775-052A-57	Sequence 57, Appl
100	3	27.3	11	4	US-09-344-525-3	Sequence 3, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-528-200-172

; Sequence 172, Application US/09528200

; Patent No. 6630570

; GENERAL INFORMATION:

; APPLICANT: LICHA, KAI

; APPLICANT: BECKER, ANDREAS

; APPLICANT: SEMMLER, WOLFHARD

; APPLICANT: WEIDENMANN, BERTRAM

; APPLICANT: HESSNIUS, CARTSEN

; APPLICANT: VOLKMER-ENGERT, RUDOLF

; APPLICANT: SCHNEIDER-MERGENER, JENS

; APPLICANT: BHARGAVA, SARAH

; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA

; TITLE OF INVENTION: FOR OPTICAL DIAGNOSIS

; FILE REFERENCE: SCH-1731

; CURRENT APPLICATION NUMBER: US/09/528,200

; CURRENT FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: DE 199 17 713.9

; PRIOR FILING DATE: 1999-09-04

; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 172  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-528-200-172

Query Match 36.4%; Score 4; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPRR 10  
||||  
Db 6 KPRR 9

RESULT 2

US-07-666-719-18

; Sequence 18, Application US/07666719

; Patent No. 5247067

; GENERAL INFORMATION:

; APPLICANT: ARIMA, Terukatsu

; APPLICANT: YAMADA, Kyoko

; APPLICANT: HATANAKA, Tadashi

; APPLICANT: NAMBA, Toshihiko

; APPLICANT: TSUJI, Masao

; TITLE OF INVENTION: PEPTIDE AND ITS USE

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: US

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/666,719

; FILING DATE: 19910422

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Oblon, No. 5247067man F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 363-264-0X

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)521-5940

; TELEFAX: (703)486-2347

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-666-719-18

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 9 KPR 11

RESULT 3

US-07-755-161A-9

; Sequence 9, Application US/07755161A  
; Patent No. 5304633  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/755,161A  
; FILING DATE: 19910905  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single

```

;   TOPOLOGY:  linear
;   MOLECULE TYPE:
;   HYPOTHETICAL:
;   ANTI-SENSE:
;   FRAGMENT TYPE:
;   ORIGINAL SOURCE:
;   ORGANISM:
;   STRAIN:
;   INDIVIDUAL ISOLATE:
;   DEVELOPMENTAL STAGE:
;   HAPLOTYPE:
;   TISSUE TYPE:
;   CELL TYPE:
;   CELL LINE:
;   ORGANELLE:
;   IMMEDIATE SOURCE:
;   LIBRARY:
;   CLONE:
;   POSITION IN GENOME:
;   CHROMOSOME/SEGMENT:
;   MAP POSITION:
;   UNITS:
;   FEATURE:
;   NAME/KEY:  modified site
;   LOCATION:  10
;   IDENTIFICATION METHOD:
;   OTHER INFORMATION:  /note= "thiol group of
;   OTHER INFORMATION:  Cys residue at location 10 connected by disulfide
bond with
;   OTHER INFORMATION:  thiol group of Cys residue at location 35 of SEQ ID
NO. 8"
;   PUBLICATION INFORMATION:
;   AUTHORS:
;   TITLE:
;   JOURNAL:
;   VOLUME:
;   ISSUE:
;   PAGES:
;   DATE:
;   DOCUMENT NUMBER:
;   FILING DATE:
;   PUBLICATION DATE:
;   RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-9

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy          9 RRS 11
            |||
Db          4 RRS 6

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RESULT 4
US-07-891-174-9
; Sequence 9, Application US/07891174

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; Patent No. 5317084  
; GENERAL INFORMATION:  
; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: Antimicrobial Peptides and an  
; TITLE OF INVENTION: Antimicrobial Agent  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500Kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: DisplayWrite  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/891,174  
; FILING DATE: 29-MAY-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/755,161  
; FILING DATE: 05-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX: 202-371-8856  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE:  
; HYPOTHETICAL:  
; ANTI-SENSE:  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; ORGANISM:  
; STRAIN:  
; INDIVIDUAL ISOLATE:  
; DEVELOPMENTAL STAGE:  
; HAPLOTYPE:  
; TISSUE TYPE:  
; CELL TYPE:  
; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:

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;   CHROMOSOME/SEGMENT:
;   MAP POSITION:
;   UNITS:
;   FEATURE:
;   NAME/KEY:  modified site
;   LOCATION:  10
;   IDENTIFICATION METHOD:
;   OTHER INFORMATION:  /note= "thiol group of
;   OTHER INFORMATION:  Cys residue at location 10 connected by disulfide
bond with
;   OTHER INFORMATION:  thiol group of Cys residue at location 35 of SEQ ID
NO. 8"
;   PUBLICATION INFORMATION:
;   AUTHORS:
;   TITLE:
;   JOURNAL:
;   VOLUME:
;   ISSUE:
;   PAGES:
;   DATE:
;   DOCUMENT NUMBER:
;   FILING DATE:
;   PUBLICATION DATE:
;   RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-9

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Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          9 RRS 11
            |||
Db          4 RRS 6

```

```

RESULT 5
US-08-046-538-1
; Sequence 1, Application US/08046538
; Patent No. 5444074
; GENERAL INFORMATION:
;   APPLICANT:  BAKER, RAYMOND
;   APPLICANT:  LADDUWAHETTY, TAMARA
;   APPLICANT:  SEWARD, EILEEN M.
;   APPLICANT:  SWAIN, CHRISTOPHER J.
;   TITLE OF INVENTION:  AZACYCLIC COMPOUNDS
;   NUMBER OF SEQUENCES:  3
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  MERCK & CO., INC.
;   STREET:    P.O. BOX 2000, 126 E. LINCOLN AVE.
;   CITY:      RAHWAY
;   STATE:     NJ
;   COUNTRY:   USA
;   ZIP:       07065
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:    IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS

```



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;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/046,538
;   FILING DATE: 19930413
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: NORTH, ROBERT J.
;   REGISTRATION NUMBER: 27,366
;   REFERENCE/DOCKET NUMBER: T-1157Y
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 908-594-7262
;   TELEX: 908-594-4720
;   INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-046-538-1

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 KPR 9
        |||
Db      9 KPR 11

```

RESULT 6

US-08-197-795-5

```

; Sequence 5, Application US/08197795
; Patent No. 5457182
; GENERAL INFORMATION:
;   APPLICANT: Wiederrecht, Gregory J.
;   APPLICANT: Sewell, Tonya J.
;   TITLE OF INVENTION: FK-506 CYTOSOLIC BINDING PROTEIN
;   NUMBER OF SEQUENCES: 21
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Merck & Co., Inc.
;   STREET: 126 E. Lincoln Avenue
;   CITY: Rahway
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07065
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/197,795
;   FILING DATE:
;   CLASSIFICATION: 530
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Thies, J. Eric

```

; REGISTRATION NUMBER: 35,382  
 ; REFERENCE/DOCKET NUMBER: 19181  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (908) 594-3904  
 ; TELEFAX: (908) 594-4720  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 US-08-197-795-5

Query Match 27.3%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQK 4  
 |||  
 Db 5 RQK 7

# RESULT 7

US-08-128-971B-15  
 ; Sequence 15, Application US/08128971B  
 ; Patent No. 5525503  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Christopher E. Rudd  
 ; APPLICANT: Prasad Kanteti  
 ; TITLE OF INVENTION: SIGNAL TRANSDUCTION VIA CD28  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: U.S.A.  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX  
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)  
 ; SOFTWARE: WordPerfect (Version 5.1)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/128,971B  
 ; FILING DATE: September 28, 1993  
 ; CLASSIFICATION: 800  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Janis K. Fraser  
 ; REGISTRATION NUMBER: 34,819  
 ; REFERENCE/DOCKET NUMBER: 00530/073001

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-128-971B-15

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 9 PRR 11

RESULT 8

US-08-470-187-3

; Sequence 3, Application US/08470187  
; Patent No. 5532152  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine E.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
; TITLE OF INVENTION: Hydrolase  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/470,187  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5532152and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 31672

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-470-187-3

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 1 MKP 3

RESULT 9

US-08-318-905-3

; Sequence 3, Application US/08318905  
; Patent No. 5641669  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl  
; TITLE OF INVENTION: Hydrolase  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,905  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 6-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5641669and, Greta E.  
; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 32205  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-318-905-3

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 1 MKP 3

RESULT 10

US-08-483-232-3

; Sequence 3, Application US/08483232  
; Patent No. 5656431  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,232  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803

; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 565643land, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32689  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-483-232-3

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 1 MKP 3

RESULT 11

US-08-256-771-32

; Sequence 32, Application US/08256771  
; Patent No. 5656591

; GENERAL INFORMATION:

; APPLICANT: Mamoru TOMITA et al.  
; TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING  
; TITLE OF INVENTION: PRODUCTS THEREWITH  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/256,771  
; FILING DATE: July 22, 1994  
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367

```

; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "Cys at position 10 is linked to
; OTHER INFORMATION: Cys at position 35 of SEQ ID No. 5656591 10 by
disulfide bond"
US-08-256-771-32

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 RRS 11
        |||
Db      4 RRS 6

```

```

RESULT 12
US-08-462-917-10
; Sequence 10, Application US/08462917
; Patent No. 5661008
; GENERAL INFORMATION:
; APPLICANT: ALMSTEDT, Annelie B
; APPLICANT: GRAY (HELLSTROM), Eva Maria
; APPLICANT: LIND, Peter
; APPLICANT: LJUNG, Catherine
; APPLICANT: SANDBERG, Helena Inga
; APPLICANT: SPIRA, Jack
; APPLICANT: SYDOW-BACKMAN, Mona
; APPLICANT: WIMAN, Helena
; TITLE OF INVENTION: RECOMBINANT HUMAN FACTOR VIII
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/462,917
;   FILING DATE:
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/934,495
;   FILING DATE:  17-DEC-1992
;   APPLICATION NUMBER:  SE 9100799-7
;   FILING DATE:  15-MAR-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Crane-Feury, Sharon E
;   REGISTRATION NUMBER:  36,113
;   REFERENCE/DOCKET NUMBER:  003300-283
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (703) 836-6620
;   TELEFAX:  (703) 836-2021
;   INFORMATION FOR SEQ ID NO:  10:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
US-08-462-917-10

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      8 PRR 10
      |||
Db      3 PRR 5

```

# RESULT 13

US-08-483-140-3

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; Sequence 3, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
;   APPLICANT:  ICOS Corporation
;   TITLE OF INVENTION:  Platelet-Activating Factor Acetyl
;   TITLE OF INVENTION:  Hydrolase
;   NUMBER OF SEQUENCES:  30
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Marshall, O'Toole, Gertein, Murray & Borun
;   STREET:  6300 Sears Tower, 233 South Wacker Drive
;   CITY:  Chicago
;   STATE:  Illinois
;   COUNTRY:  USA
;   ZIP:  60606
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/483,140  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 6-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 6-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5698403and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32781  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-483-140-3

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MKP 8  
|||  
Db 1 MKP 3

RESULT 14

US-08-323-531-32

; Sequence 32, Application US/08323531  
; Patent No. 5731188  
; GENERAL INFORMATION:  
; APPLICANT: Cochran Ph.D., Mark D  
; TITLE OF INVENTION: Recombinant Equine Herpesvirus  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/323,531  
; FILING DATE:

; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/926,784  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-323-531-32

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 4 PRR 6

RESULT 15

US-08-548-540-145

; Sequence 145, Application US/08548540  
; Patent No. 5733731  
; GENERAL INFORMATION:  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Cull, Millard G.  
; APPLICANT: Miller, Jeff F.  
; APPLICANT: Stemmer, Willem P.C.  
; APPLICANT: Gates, Christian M.  
; TITLE OF INVENTION: Peptide Library and Screening Method  
; NUMBER OF SEQUENCES: 162  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/548,540  
; FILING DATE: 26-OCT-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/290,641

```

; FILING DATE: 15-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 145:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-548-540-145

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 RRS 11
        |||
Db      5 RRS 7

```

# RESULT 16

US-08-548-540-160

```

; Sequence 160, Application US/08548540
; Patent No. 5733731
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, Millard G.
; APPLICANT: Miller, Jeff F.
; APPLICANT: Stemmer, Willem P.C.
; APPLICANT: Gates, Christian M.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/548,540
; FILING DATE: 26-OCT-1995
; CLASSIFICATION: 435

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,641
; FILING DATE: 15-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,321
; FILING DATE: 15-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528J-001240US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-548-540-160

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 RRS 11
            |||
Db          5 RRS 7

```

# RESULT 17

US-08-198-094-32

```

; Sequence 32, Application US/08198094
; Patent No. 5741696
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Mark D
; TITLE OF INVENTION: Recombinant Equine Herpesvirus
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/198,094
; FILING DATE: February 17, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P

```

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-198-094-32

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 4 PRR 6

RESULT 18

US-08-702-970-2

; Sequence 2, Application US/08702970  
; Patent No. 5759787  
; GENERAL INFORMATION:  
; APPLICANT: Strulovici, Berta  
; TITLE OF INVENTION: Kinase Assay  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/702,970  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brezner, David J  
; REGISTRATION NUMBER: 24,7747  
; REFERENCE/DOCKET NUMBER: T96-007/64444  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
US-08-702-970-2

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 9 RRS 11

RESULT 19

US-08-381-984-32

; Sequence 32, Application US/08381984

; Patent No. 5804555

; GENERAL INFORMATION:

; APPLICANT: Mamoru TOMITA et al.

; TITLE OF INVENTION: ANTIOXIDANT

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/381,984

; FILING DATE: April 11, 1995

; CLASSIFICATION: 252

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY:

```

; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "the specified peptide as well as
; OTHER INFORMATION: peptides including the specified peptide as a
fragment thereof"
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: /note= "cysteine residues at position 10
; OTHER INFORMATION: is linked by disulfide linkage with the cysteine
residue at pos
; OTHER INFORMATION: SEQ ID No. 5804555 29"
US-08-381-984-32

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 RRS 11
            |||
Db          4 RRS 6

```

# RESULT 20

```

US-08-669-721-16
; Sequence 16, Application US/08669721
; Patent No. 5834236
; GENERAL INFORMATION:
; APPLICANT: Lamb et al., Christopher J.
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,721
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellison, Eldora L.
; REGISTRATION NUMBER: 39,967
; REFERENCE/DOCKET NUMBER: 07251/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 16:

```

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-669-721-16

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 4 KPR 6

RESULT 21

US-08-485-938A-3

; Sequence 3, Application US/08485938A  
; Patent No. 5847088

; GENERAL INFORMATION:

; APPLICANT: Cousens, Lawrence S.  
; APPLICANT: Eberhardt, Christine D.  
; APPLICANT: Gray, Patrick W.  
; APPLICANT: Le Trong, Hai  
; APPLICANT: Tjoelker, Larry W.  
; APPLICANT: Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; TITLE OF INVENTION: Acetylhydrolase  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/485,938A  
; FILING DATE:  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5847088and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32792



; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-485-938A-3

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 1 MKP 3

RESULT 22

US-08-464-182A-11

; Sequence 11, Application US/08464182A  
; Patent No. 5849885  
; GENERAL INFORMATION:  
; APPLICANT: Nuijens, Jan H.  
; APPLICANT: Van Veen, Harry H.  
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,182A  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/406,271  
; FILING DATE: 09-MAR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/198,321  
; FILING DATE: 16-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 016994-004920US

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 326-2400
; TELEFAX: (650) 326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Calbio. peak II"
US-08-464-182A-11

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 RRS 11
        |||
Db      2 RRS 4

```

# RESULT 23

```

US-08-464-182A-12
; Sequence 12, Application US/08464182A
; Patent No. 5849885
; GENERAL INFORMATION:
; APPLICANT: Nuijens, Jan H.
; APPLICANT: Van Veen, Harry H.
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,182A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,271
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994

```

```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Apple, Randolph T.
;   REGISTRATION NUMBER: 36,429
;   REFERENCE/DOCKET NUMBER: 016994-004920US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 326-2400
;   TELEFAX: (650) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 11 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: not relevant
;     TOPOLOGY: not relevant
;   MOLECULE TYPE: peptide
;   FEATURE:
;     NAME/KEY: Peptide
;     LOCATION: 1..11
;   OTHER INFORMATION: /note= "Calbio. peak I"
US-08-464-182A-12

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      9 RRS 11
        |||
Db      1 RRS 3

```

# RESULT 24

US-08-693-274A-3

```

; Sequence 3, Application US/08693274A
; Patent No. 5861491
; GENERAL INFORMATION:
;   APPLICANT: Nuijens, Jan H.
;   APPLICANT: Van Veen, Harry H.
;   TITLE OF INVENTION: Isolation of Lactoferrin from Milk
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Townsend and Townsend and Crew LLP
;     STREET: Two Embarcadero Center, Eighth Floor
;     CITY: San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94111-3834
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/693,274A
;     FILING DATE: 16-OCT-1996
;     CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/464,182
;     FILING DATE: 05-JUN-1995

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,271
; FILING DATE: 09-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00583
; FILING DATE: 16-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016994-004930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "hLF Calbi.peakII N-terminus"
US-08-693-274A-3

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 RRS 11
        |||
Db      2 RRS 4

```

# RESULT 25

```

US-08-693-274A-4
; Sequence 4, Application US/08693274A
; Patent No. 5861491
; GENERAL INFORMATION:
; APPLICANT: Nuijens, Jan H.
; APPLICANT: Van Veen, Harry H.
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/693,274A
;   FILING DATE:  16-OCT-1996
;   CLASSIFICATION:  530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/464,182
;   FILING DATE:  05-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/406,271
;   FILING DATE:  09-MAR-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  WO PCT/EP95/00583
;   FILING DATE:  16-FEB-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/198,321
;   FILING DATE:  16-FEB-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Apple, Randolph T.
;   REGISTRATION NUMBER:  36,429
;   REFERENCE/DOCKET NUMBER:  016994-004930US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 576-0200
;   TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   FEATURE:
;   NAME/KEY:  Peptide
;   LOCATION:  1..11
;   OTHER INFORMATION:  /note= "hLF Calbi.peakI N-terminus"
US-08-693-274A-4

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          9 RRS 11
            |||
Db          1 RRS 3

```

# RESULT 26

```

US-08-637-759B-211
; Sequence 211, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT:  David William Holden
; TITLE OF INVENTION:  Identification of Genes
; NUMBER OF SEQUENCES:  501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Patrea L. Pabst

```

; STREET: 2800 One Atlantic Center  
 ; STREET: 1201 West Peachtree Street  
 ; CITY: Atlanta  
 ; STATE: Georgia  
 ; COUNTRY: USA  
 ; ZIP: 30309-3450  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/637,759B  
 ; FILING DATE: 03-MAY-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB95/02875  
 ; FILING DATE: 11-DEC-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pabst, Patrea L.  
 ; REGISTRATION NUMBER: 31,284  
 ; REFERENCE/DOCKET NUMBER: RPMS 101  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (404) 873-8794  
 ; TELEFAX: (404) 873-8795  
 ; INFORMATION FOR SEQ ID NO: 211:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 US-08-637-759B-211

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
 |||  
 Db 4 PRR 6

RESULT 27  
 US-08-679-865-35  
 ; Sequence 35, Application US/08679865  
 ; Patent No. 5912137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tsien, Roger Y.  
 ; APPLICANT: Cubitt, Andrew B.  
 ; TITLE OF INVENTION: Assays for Protein Kinases Using  
 ; TITLE OF INVENTION: Fluorescent Protein Substrates  
 ; NUMBER OF SEQUENCES: 48  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP

```

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,865
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John S.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 02307Z-069000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-679-865-35

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 RRS 11
            |||
Db          4 RRS 6

```

```

RESULT 28
US-08-727-688-24
; Sequence 24, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D377/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

```

```

;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/727,688
;   FILING DATE:
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Porembski, Priscilla E.
;   REGISTRATION NUMBER:  33,207
;   REFERENCE/DOCKET NUMBER:  5967.US.01
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (847) 937-0378
;   TELEFAX:  (847) 938-2623
;   TELEX:
;   INFORMATION FOR SEQ ID NO:  24:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  No. 5919638e
US-08-727-688-24

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      8 PRR 10
      |||
Db      7 PRR 9

```

```

RESULT 29
US-08-406-271-11
; Sequence 11, Application US/08406271
; Patent No. 5919913
; GENERAL INFORMATION:
; APPLICANT:  Nuyens, Jan H.
; APPLICANT:  Van Veen, Harry H.
; TITLE OF INVENTION:  Isolation of Lactoferrin from Milk
; NUMBER OF SEQUENCES:  28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
; STREET:  One Market Plaza, Steuart Street Tower, 20th
; STREET:  Floor
; CITY:  San Francisco
; STATE:  CA
; COUNTRY:  USA
; ZIP:  94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  PatentIn Release #1.0, Version #1.30

```



```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,271
; FILING DATE: 09-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,321
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016994-004910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Calbio. peak II"
US-08-406-271-11

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      9 RRS 11
      |||
Db      2 RRS 4

```

RESULT 30

US-08-406-271-12

```

; Sequence 12, Application US/08406271
; Patent No. 5919913
; GENERAL INFORMATION:
; APPLICANT: Nuyens, Jan H.
; APPLICANT: Van Veen, Harry H.
; TITLE OF INVENTION: Isolation of Lactoferrin from Milk
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/406,271
;   FILING DATE:  09-MAR-1995
;   CLASSIFICATION:  530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/198,321
;   FILING DATE:  16-FEB-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Apple, Randolph T.
;   REGISTRATION NUMBER:  36,429
;   REFERENCE/DOCKET NUMBER:  016994-004910
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 326-2400
;   TELEFAX:  (415) 326-2422
;   INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  not relevant
;   TOPOLOGY:  not relevant
;   MOLECULE TYPE:  peptide
;   FEATURE:
;   NAME/KEY:  Peptide
;   LOCATION:  1..11
;   OTHER INFORMATION:  /note= "Calbio. peak I"
US-08-406-271-12

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          9 RRS 11
            |||
Db          1 RRS 3

```

# RESULT 31

```

US-08-680-876-35
; Sequence 35, Application US/08680876
; Patent No. 5925558
; GENERAL INFORMATION:
;   APPLICANT:  Tsien, Roger Y.
;   APPLICANT:  Cubitt, Andrew B.
;   TITLE OF INVENTION:  Assays for Protein Kinases Using
;   TITLE OF INVENTION:  Fluorescent Protein Substrates
;   NUMBER OF SEQUENCES:  48
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Townsend and Townsend and Crew LLP
;   STREET:  Two Embarcadero Center, Eighth Floor
;   CITY:  San Francisco
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94111-3834
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible

```

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/680,876
;   FILING DATE:  16-JUL-1996
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Storella, John S.
;   REGISTRATION NUMBER:  32,944
;   REFERENCE/DOCKET NUMBER:  02307Z-069200
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 576-0200
;   TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  35:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-680-876-35

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          9 RRS 11
            |||
Db          4 RRS 6

```

```

RESULT 32
US-08-934-222-77
; Sequence 77, Application US/08934222
; Patent No. 5928896
;   GENERAL INFORMATION:
;   APPLICANT:  EVANS, Herbert J.
;   APPLICANT:  KINI, R. Manjunatha
;   TITLE OF INVENTION:  Polypeptides That Include Conformation-
;   TITLE OF INVENTION:  Constraining Groups Which Flank A Protein-Protein
Interaction
;   TITLE OF INVENTION:  Site
;   NUMBER OF SEQUENCES:  153
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Foley & Lardner
;   STREET:  Suite 500, 3000 K Street NW
;   CITY:  Washington
;   STATE:  DC
;   COUNTRY:  USA
;   ZIP:  20007
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/934,222

```

```
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-222-77
```

```
Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      8 PRR 10
        |||
Db      2 PRR 4
```

# RESULT 33

US-08-933-402-77

```
; Sequence 77, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-77

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 PRR 10
      |||
Db      2 PRR 4

```

```

RESULT 34
US-09-207-621-77
; Sequence 77, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein
Interaction Sit
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818

```

```

; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-77

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 PRR 10
      |||
Db      2 PRR 4

```

```

RESULT 35
US-08-532-818-77
; Sequence 77, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-532-818-77

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      8 PRR 10
        |||
Db      2 PRR 4

```

# RESULT 36

US-08-910-041-3

```

; Sequence 3, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:

```

```

; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-910-041-3

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      6 MKP 8
        |||
Db      1 MKP 3

```

# RESULT 37

```

US-08-871-355A-211
; Sequence 211, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```



```

; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-211

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 PRR 10
        |||
Db      4 PRR 6

```

RESULT 38

US-08-159-339A-1139

; Sequence 1139, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

```

; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1139

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      8 PRR 10
        |||
Db      5 PRR 7

```

```

RESULT 39
US-09-328-474-3
; Sequence 3, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

```

```

; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-328-474-3

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 MKP 8
      |||
Db      1 MKP 3

```

# RESULT 40

US-09-231-797-77

; Sequence 77, Application US/09231797

; Patent No. 6084066

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Proten-Protein  
Interaction Sit

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20007  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/231,797  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/532,818  
 ; FILING DATE: 03-MAY-1996  
 ; APPLICATION NUMBER: PCT/US94/04294  
 ; FILING DATE: 21-APR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: U.S. 08/143,364  
 ; FILING DATE: 29-OCT-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: U.S. 08/051,741  
 ; FILING DATE: 23-APR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Isacson, John P.  
 ; REGISTRATION NUMBER: 33,751  
 ; REFERENCE/DOCKET NUMBER: 040433/0148  
 ; INFORMATION FOR SEQ ID NO: 77:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 US-09-231-797-77

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
 |||  
 Db 2 PRR 4

RESULT 41  
 US-08-609-236-5  
 ; Sequence 5, Application US/08609236  
 ; Patent No. 6087398  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Steven R. Goodman  
 ; TITLE OF INVENTION: No. 6087398e1 Sickel Cell Anemia Treatment  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McGregor & Adler, LLP  
 ; STREET: 8011 Candle Lane  
 ; CITY: Houston  
 ; STATE: Texas

```

; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,236
; FILING DATE: March 1, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/002,288
; FILING DATE: August 14, 1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5807
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: Amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; MOLECULE TYPE:
; DESCRIPTION: Peptide
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
US-08-609-236-5

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      5 TMK 7
      |||
Db      9 TMK 11

```

```

RESULT 42
US-09-100-546-3
; Sequence 3, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.

```

; APPLICANT: Eberhardt, Christine D.  
 ; APPLICANT: Gray, Patrick W.  
 ; APPLICANT: Le Trong, Hai  
 ; APPLICANT: Tjoelker, Larry W.  
 ; APPLICANT: Wilder, Cheryl L.  
 ; TITLE OF INVENTION: Platelet-Activating Factor  
 ; TITLE OF INVENTION: Acetylhydrolase  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/100,546  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/010,715  
 ; FILING DATE:  
 ; APPLICATION NUMBER: US 08/318,905  
 ; FILING DATE: 06-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/133,803  
 ; FILING DATE: 06-OCT-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 6099836and, Greta E.  
 ; REGISTRATION NUMBER: 35,302  
 ; REFERENCE/DOCKET NUMBER: 27866/32793  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312) 474-6300  
 ; TELEFAX: (312) 474-0448  
 ; TELEX: 25-3658  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-09-100-546-3

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
 |||  
 Db 1 MKP 3

RESULT 43

US-08-934-224-77

; Sequence 77, Application US/08934224

; Patent No. 6100044

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

; TITLE OF INVENTION: Site

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/934,224

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; APPLICATION NUMBER: PCT/US94/04294

; FILING DATE: 21-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Isacson, John P.

; REGISTRATION NUMBER: 33,751

; REFERENCE/DOCKET NUMBER: 040433/0148

; INFORMATION FOR SEQ ID NO: 77:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-934-224-77

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10

|||

Db 2 PRR 4

RESULT 44  
 US-08-933-843-77  
 ; Sequence 77, Application US/08933843  
 ; Patent No. 6111069  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EVANS, Herbert J.  
 ; APPLICANT: KINI, R. Manjunatha  
 ; TITLE OF INVENTION: Polypeptides That Include Conformation-  
 ; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein  
 Interaction  
 ; TITLE OF INVENTION: Site  
 ; NUMBER OF SEQUENCES: 153  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: Suite 500, 3000 K Street NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20007  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/933,843  
 ; FILING DATE: 19-SEPT-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/532,818  
 ; FILING DATE: 03-MAY-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: U.S. 08/143,364  
 ; FILING DATE: 29-OCT-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: U.S. 08/051,741  
 ; FILING DATE: 23-APR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Isacson, John P.  
 ; REGISTRATION NUMBER: 33,751  
 ; REFERENCE/DOCKET NUMBER: 040433/0148  
 ; INFORMATION FOR SEQ ID NO: 77:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 US-08-933-843-77

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
 |||  
 Db 2 PRR 4



RESULT 45  
 US-09-010-715-3  
 ; Sequence 3, Application US/09010715  
 ; Patent No. 6146625  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cousens, Lawrence S.  
 ; APPLICANT: Eberhardt, Christine D.  
 ; APPLICANT: Gray, Patrick W.  
 ; APPLICANT: Le Trong, Hai  
 ; APPLICANT: Tjoelker, Larry W.  
 ; APPLICANT: Wilder, Cheryl L.  
 ; TITLE OF INVENTION: Platelet-Activating Factor  
 ; TITLE OF INVENTION: Acetylhydrolase  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/010,715  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/318,905  
 ; FILING DATE: 06-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/133,803  
 ; FILING DATE: 06-OCT-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 6146625and, Greta E.  
 ; REGISTRATION NUMBER: 35,302  
 ; REFERENCE/DOCKET NUMBER: 27866/32793  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312) 474-6300  
 ; TELEFAX: (312) 474-0448  
 ; TELEX: 25-3658  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-09-010-715-3

Query Match 27.3%; Score 3; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8

Db                    |||  
                      1 MKP 3

RESULT 46  
US-08-934-223-77  
; Sequence 77, Application US/08934223  
; Patent No. 6147189  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein  
Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,223  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/532,818  
; FILING DATE: 03-MAY-1996  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Isacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-934-223-77

Query Match                    27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity       100.0%; Pred. No. 1.7e+03;  
Matches       3; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy 8 PRR 10  
|||  
Db 2 PRR 4

RESULT 47

US-08-836-075A-107

; Sequence 107, Application US/08836075A

; Patent No. 6180768

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT

; APPLICANT: STUYVER, LIEVEN

; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND

DIAGNOSTIC

; TITLE OF INVENTION: AGENTS

; NUMBER OF SEQUENCES: 207

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARNOLD, WHITE & DURKEE

; STREET: P.O. BOX 4433

; CITY: HOUSTON

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Microsoft Word 6.0 / ASCII text output

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/836,075A

; FILING DATE: 21 Apr 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP95/04155

; FILING DATE: 23 Oct 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 94870166.9

; FILING DATE: 21 Oct 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95870076.7

; FILING DATE: 28 Jun 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KAMMERER, PATRICIA A.

; REGISTRATION NUMBER: 29,775

; REFERENCE/DOCKET NUMBER: INNS:004

; INFORMATION FOR SEQ ID NO: 107:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-836-075A-107

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 1 ARQ 3

RESULT 48

US-08-836-075A-108

; Sequence 108, Application US/08836075A  
; Patent No. 6180768  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: STUYVER, LIEVEN  
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES  
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND  
DIAGNOSTIC

; TITLE OF INVENTION: AGENTS  
; NUMBER OF SEQUENCES: 207  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARNOLD, WHITE & DURKEE  
; STREET: P.O. BOX 4433  
; CITY: HOUSTON  
; STATE: TEXAS  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Microsoft Word 6.0 / ASCII text output  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/836,075A  
; FILING DATE: 21 Apr 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP95/04155  
; FILING DATE: 23 Oct 1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 94870166.9  
; FILING DATE: 21 Oct 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95870076.7  
; FILING DATE: 28 Jun 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KAMMERER, PATRICIA A.  
; REGISTRATION NUMBER: 29,775  
; REFERENCE/DOCKET NUMBER: INNS:004  
; INFORMATION FOR SEQ ID NO: 108:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-836-075A-108

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 2 RRS 4

RESULT 49

US-08-602-999A-290

; Sequence 290, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 290:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-290

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10

Db

|||  
8 PRR 10

RESULT 50

US-08-652-877-41

; Sequence 41, Application US/08652877

; Patent No. 6187548

; GENERAL INFORMATION:

; APPLICANT: Akerstrom, Goran

; APPLICANT: Juhlin, Claes

; APPLICANT: Rask, Lars

; APPLICANT: Crumley, Gregg R.

; APPLICANT: Morse, Clarence C.

; APPLICANT: Murray, Edward M.

; APPLICANT: Hjalms, Goran

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments

; TITLE OF INVENTION: Thereof and DNA Encoding Same

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Rd., 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426-0107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: System 7.5.1

; SOFTWARE: Word 6.0 (Patentin)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,877

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/15203

; FILING DATE: 22-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/344,836

; FILING DATE: 23-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/487,314

; FILING DATE: 07-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Savitzky, Martin

; REGISTRATION NUMBER: 29,699

; REFERENCE/DOCKET NUMBER: A1355E-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-454-3816

; TELEFAX: 610-454-3808

; INFORMATION FOR SEQ ID NO: 41:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-652-877-41

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 9 MKP 11

RESULT 51

US-09-189-344-16

; Sequence 16, Application US/09189344  
; Patent No. 6191258  
; GENERAL INFORMATION:  
; APPLICANT: Lamb et al., Christopher J.  
; TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/189,344  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/669,721  
; FILING DATE: 27-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ellison, Eldora L.  
; REGISTRATION NUMBER: 39,967  
; REFERENCE/DOCKET NUMBER: 07251/014001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-189-344-16

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 4 KPR 6

RESULT 52

US-09-577-758-3

; Sequence 3, Application US/09577758

; Patent No. 6203790

; GENERAL INFORMATION:

; APPLICANT: Cousens, Lawrence S.

; APPLICANT: Eberhardt, Christine D.

; APPLICANT: Gray, Patrick W.

; APPLICANT: Le Trong, Hai

; APPLICANT: Tjoelker, Larry W.

; APPLICANT: Wilder, Cheryl L.

; TITLE OF INVENTION: Platelet-Activating Factor

; TITLE OF INVENTION: Acetylhydrolase

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/577,758

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/010,715

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/133,803

; FILING DATE: 06-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6203790and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/32793

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3658

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids



; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-577-758-3

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 1 MKP 3

RESULT 53

US-09-208-966-4

; Sequence 4, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-208-966-4

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 6 ARQ 8

RESULT 54

US-09-208-966-40

; Sequence 40, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20

; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-208-966-40

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 6 ARQ 8

RESULT 55  
US-09-208-966-55  
; Sequence 55, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-208-966-55

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 8 PRR 10

RESULT 56  
US-09-208-966-56  
; Sequence 56, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF

; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-208-966-56

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 5 PRR 7

RESULT 57

US-09-208-966-57  
; Sequence 57, Application US/09208966  
; Patent No. 6221355  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/208,966  
; CURRENT FILING DATE: 1998-12-10  
; EARLIER APPLICATION NUMBER: 60/082,402  
; EARLIER FILING DATE: 1998-04-20  
; EARLIER APPLICATION NUMBER: 60/069,012  
; EARLIER FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-208-966-57

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 5 PRR 7

RESULT 58

US-08-107-794A-32

```

; Sequence 32, Application US/08107794A
; Patent No. 6225111
; GENERAL INFORMATION:
;   APPLICANT: Cochran, Mark D.
;   APPLICANT: Chang, Christina H.
;   TITLE OF INVENTION: Recombinant Equine Herpesvirus
;   NUMBER OF SEQUENCES: 71
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: John P. White
;     STREET: 1185 Avenue of Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: USA
;     ZIP: 10036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/107,794A
;     FILING DATE: February 7, 1995
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: White, John P
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212)278-0422
;     TELEFAX: (212)391-0525
;   INFORMATION FOR SEQ ID NO: 32:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-107-794A-32

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 PRR 10
      |||
Db      4 PRR 6

```

```

RESULT 59
US-08-476-515A-41
; Sequence 41, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
;   APPLICANT: Akerstrom, Goran
;   APPLICANT: Juhlin, Claes
;   APPLICANT: Rask, Lars
;   APPLICANT: Crumley, Gregg R.
;   APPLICANT: Morse, Clarence C.
;   APPLICANT: Murray, Edward M.
;   APPLICANT: Hjalms, Goran

```

```

; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-476-515A-41

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 MKP 8
      |||
Db      9 MKP 11

```

RESULT 60

US-09-263-975-35  
; Sequence 35, Application US/09263975  
; Patent No. 6248550  
; GENERAL INFORMATION:  
; APPLICANT: Tsien, Roger Y.  
; APPLICANT: Cubitt, Andrew B.  
; TITLE OF INVENTION: Assays for Protein Kinases Using  
; TITLE OF INVENTION: Fluorescent Protein Substrates  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,975  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/679,865  
; FILING DATE: 16-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John S.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 02307Z-069000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-263-975-35

Query Match 27.3%; Score 3; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
| | |  
Db 4 RRS 6

RESULT 61  
US-09-413-492-77  
; Sequence 77, Application US/09413492  
; Patent No. 6258550

```

; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-413-492-77

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      8 PRR 10
      |||
Db      2 PRR 4

```

```

RESULT 62
US-09-044-411-7
; Sequence 7, Application US/09044411A

```

```

; Patent No. 6258774
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
; FILE REFERENCE: 601-1-083
; CURRENT APPLICATION NUMBER: US/09/044,411A
; CURRENT FILING DATE: 1998-03-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Same as Sequence ID 2, but with a substitution of
; Patent No. 6258774
; OTHER INFORMATION: Gln to Pro.
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Cys(biotin)
; FEATURE:
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; FEATURE:
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-044-411-7

```

```

Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      8 PRR 10
        |||
Db      6 PRR 8

```

# RESULT 63

US-09-201-945-211

```

; Sequence 211, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```



```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-201-945-211

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 PRR 10
      |||
Db      4 PRR 6

```

```

RESULT 64
US-09-227-357-423
; Sequence 423, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: PZ010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732

```

; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,931  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,932  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,916  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,930  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,918  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,920  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,733  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/052,795  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,919  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/051,928  
; EARLIER FILING DATE: 1997-07-08  
; EARLIER APPLICATION NUMBER: 60/055,722  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,723  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,948  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,949  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,953  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,950  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,947  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,964  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/056,360  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,684  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,984  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/055,954  
; EARLIER FILING DATE: 1997-08-18  
; EARLIER APPLICATION NUMBER: 60/058,785  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,664  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,660  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,661  
; EARLIER FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 423  
; LENGTH: 11

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-227-357-423

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 5 QKT 7

RESULT 65

US-09-187-859-3080  
; Sequence 3080, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3080  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-09-187-859-3080

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 7 QKT 9

RESULT 66

US-09-187-859-3125  
; Sequence 3125, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3125  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-09-187-859-3125

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 7 QKT 9

RESULT 67

US-09-187-859-3170  
; Sequence 3170, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187,859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3170  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-09-187-859-3170

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 7 QKT 9

RESULT 68

US-09-187-859-3215  
; Sequence 3215, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:

```

; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3215
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-09-187-859-3215

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 QKT 5
      |||
Db      7 QKT 9

```

RESULT 69

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US-09-187-859-3260
; Sequence 3260, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3260
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-09-187-859-3260

```

```

Query Match          27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 QKT 5
      |||
Db      7 QKT 9

```

RESULT 70

US-09-500-124-290

; Sequence 290, Application US/09500124

; Patent No. 6432920

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: KAY, Brian K.

; APPLICANT: THORN, Judith M.

; APPLICANT: QUILLIAM, Lawrence A.

; APPLICANT: DER, Channing J.

; APPLICANT: FOWLKES, Dana M.

; APPLICANT: RIDER, James E.

; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

; TITLE OF INVENTION: ISOLATING AND USING SAME

; NUMBER OF SEQUENCES: 467

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/500,124

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/602,999

; FILING DATE: 16-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-202

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 290:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-09-500-124-290

Query Match 27.3%; Score 3; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

8 PRR 10

Db                    |||  
                      8 PRR 10

RESULT 71

US-09-347-926-20  
; Sequence 20, Application US/09347926  
; Patent No. 6440386  
; GENERAL INFORMATION:  
; APPLICANT: LEUNG, SHUI-ON  
; TITLE OF INVENTION: STABILIZED RADIOPHOSPHATE-LABELED PROTEINS  
; FILE REFERENCE: 018733/0936  
; CURRENT APPLICATION NUMBER: US/09/347,926  
; CURRENT FILING DATE: 1999-07-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-347-926-20

Query Match                    27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity    100.0%; Pred. No. 1.7e+03;  
Matches        3; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

Qy                    6 MKP 8  
                      |||  
Db                    9 MKP 11

RESULT 72

US-09-588-417-5  
; Sequence 5, Application US/09588417  
; Patent No. 6458552  
; GENERAL INFORMATION:  
; APPLICANT: Fourie, Anne  
; APPLICANT: Karlsson, Lars  
; APPLICANT: Thurmond, Rob  
; TITLE OF INVENTION: Metalloprotease Peptide Substrates And Methods  
; FILE REFERENCE: ORT-1220  
; CURRENT APPLICATION NUMBER: US/09/588,417  
; CURRENT FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-588-417-5

Query Match                    27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity    100.0%; Pred. No. 1.7e+03;  
Matches        3; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

Qy 1 ARQ 3  
|||  
Db 7 ARQ 9

RESULT 73

US-09-839-743-19

; Sequence 19, Application US/09839743  
; Patent No. 6472211  
; GENERAL INFORMATION:  
; APPLICANT: The Salk Institute for Biological Sciences  
; APPLICANT: Lamb, Christopher  
; APPLICANT: Doerner, Peter  
; APPLICANT: Laible, Goetz  
; TITLE OF INVENTION: No. 6472211el Transcription Enhancer Element and  
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof  
; FILE REFERENCE: SALKINS.008DV3  
; CURRENT APPLICATION NUMBER: US/09/839,743  
; CURRENT FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: US 09/401,336  
; PRIOR FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: US 09/189,344  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 08/669,721  
; PRIOR FILING DATE: 1996-06-27  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Nicotiana tabacum  
US-09-839-743-19

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 4 KPR 6

RESULT 74

US-09-260-629-15

; Sequence 15, Application US/09260629  
; Patent No. 6479626  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jin-Soo  
; APPLICANT: Pabo, Carl O.  
; APPLICANT: Massachusetts Institute of Technology  
; TITLE OF INVENTION: Poly Zinc Finger Proteins With Improved Linkers  
; FILE REFERENCE: 019496-002510US  
; CURRENT APPLICATION NUMBER: US/09/260,629  
; CURRENT FILING DATE: 1999-03-01  
; EARLIER APPLICATION NUMBER: US 60/076,454  
; EARLIER FILING DATE: 1998-03-02



; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:longer flexible  
; OTHER INFORMATION: linker for fusion protein 268//NRE containing a  
; OTHER INFORMATION: Gly-Gly-Gly-Ser sequence  
US-09-260-629-15

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQK 4  
|||  
Db 1 RQK 3

RESULT 75

US-09-129-192C-35  
; Sequence 35, Application US/09129192C  
; Patent No. 6495664  
; GENERAL INFORMATION:  
; APPLICANT: Aurora Biosciences Corporation  
; APPLICANT: Cubitt, Andrew B.  
; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational  
Modifications  
; FILE REFERENCE: AURO1270 (08366/031001)  
; CURRENT APPLICATION NUMBER: US/09/129,192C  
; CURRENT FILING DATE: 1998-07-24  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: phosphorylation site inserted at the N-terminus  
US-09-129-192C-35

Query Match 27.3%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 4 RRS 6

Search completed: April 8, 2004, 15:52:10  
Job time : 12.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds  
(without alignments)  
122.816 Million cell updates/sec

Title: US-09-787-443A-12  
Perfect score: 11  
Sequence: 1 ARQKTMKPRRS 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query		Match	Length	DB	ID	Description
	Score	%					
1	3	27.3	11	2	S23308	substance P - rain	
2	3	27.3	11	2	S23306	substance P - Atla	
3	3	27.3	11	2	S66606	quinoline 2-oxidor	
4	3	27.3	11	2	S33300	probable substance	
5	3	27.3	11	2	PH1583	Ig H chain V-D-J r	
6	2	18.2	11	1	XASNBA	bradykinin-potenti	
7	2	18.2	11	1	SPHO	substance P - hors	
8	2	18.2	11	1	A60654	substance P - guin	
9	2	18.2	11	2	G42762	proteasome endopep	
10	2	18.2	11	2	A33917	dihydroorotase (EC	
11	2	18.2	11	2	JN0023	substance P - chic	
12	2	18.2	11	2	S32575	ribosomal protein	
13	2	18.2	11	2	A57458	gene Gax protein -	

14	2	18.2	11	2	A61033	ranatachykinin A -
15	2	18.2	11	2	D61033	ranatachykinin D -
16	2	18.2	11	2	S42449	ant1 protein - pha
17	2	18.2	11	2	JQ0395	hypothetical prote
18	2	18.2	11	2	PQ0231	beta-glucosidase (
19	2	18.2	11	2	S42587	celF protein - Esc
20	2	18.2	11	2	B43669	hypothetical prote
21	2	18.2	11	2	PC2372	58K heat shock pro
22	2	18.2	11	2	B41835	translation elonga
23	2	18.2	11	2	E41476	probable antigen 5
24	2	18.2	11	2	S33519	probable secreted
25	2	18.2	11	2	H54346	pyruvate synthase
26	2	18.2	11	2	T06383	hypothetical prote
27	2	18.2	11	2	JQ2307	hypothetical 1.5K
28	2	18.2	11	2	JQ2317	hypothetical 1.5K
29	2	18.2	11	2	S78026	ribosomal protein
30	2	18.2	11	2	A34135	DNA-binding protei
31	2	18.2	11	2	A26120	6-phosphofructokin
32	2	18.2	11	2	C37196	bradykinin-potenti
33	2	18.2	11	2	D37196	bradykinin-potenti
34	2	18.2	11	2	PT0302	Ig heavy chain CRD
35	2	18.2	11	2	I54193	Rhesus blood group
36	2	18.2	11	2	S68637	acetylcholinestera
37	2	18.2	11	2	D56979	collagen alpha 1(I
38	2	18.2	11	2	A33571	folliculin - bovi
39	2	18.2	11	2	A14454	6-phosphofructokin
40	2	18.2	11	2	PH1632	Ig H chain V-D-J r
41	2	18.2	11	2	PH1600	Ig H chain V-D-J r
42	2	18.2	11	2	PH1584	Ig H chain V-D-J r
43	2	18.2	11	2	PT0214	T-cell receptor be
44	2	18.2	11	2	A49037	TcR gamma V-J regi
45	2	18.2	11	2	PD0441	translation elonga
46	2	18.2	11	2	I77447	urinary protein -
47	2	18.2	11	2	PH0939	T-cell receptor be
48	2	18.2	11	2	PH0947	T-cell receptor be
49	2	18.2	11	2	PH0919	T-cell receptor be
50	2	18.2	11	2	T12264	cytochrome-c oxida
51	2	18.2	11	2	T12253	cytochrome-c oxida
52	2	18.2	11	2	T12244	cytochrome-c oxida
53	2	18.2	11	2	T12248	cytochrome-c oxida
54	2	18.2	11	2	T17078	cytochrome-c oxida
55	2	18.2	11	2	S60294	tubulin 2 beta-3 c
56	2	18.2	11	4	I54081	retinoic acid rece
57	1	9.1	11	1	XAVIBH	bradykinin-potenti
58	1	9.1	11	1	ECLQ2M	tachykinin II - mi
59	1	9.1	11	1	EOOCC	eledoisin - curled
60	1	9.1	11	1	EOOC	eledoisin - musky
61	1	9.1	11	1	GMROL	leucosulfakinin -
62	1	9.1	11	1	LFTWWE	probable trpEG lea
63	1	9.1	11	2	S66196	alcohol dehydrogen
64	1	9.1	11	2	S68392	H+-transporting tw
65	1	9.1	11	2	B49164	chromogranin-B - r
66	1	9.1	11	2	A40693	transgelin - sheep
67	1	9.1	11	2	A38841	rhodopsin homolog
68	1	9.1	11	2	PQ0682	photosystem I 17.5
69	1	9.1	11	2	S00616	parasporal crystal
70	1	9.1	11	2	C53652	rhlR protein - Pse

71	1	9.1	11	2	S09074	cytochrome P450-4b
72	1	9.1	11	2	A26930	ermG leader peptid
73	1	9.1	11	2	D60409	kassinin-like pept
74	1	9.1	11	2	F60409	substance P-like p
75	1	9.1	11	2	E60409	substance P-like p
76	1	9.1	11	2	YHRT	morphogenetic neur
77	1	9.1	11	2	YHHU	morphogenetic neur
78	1	9.1	11	2	YHBO	morphogenetic neur
79	1	9.1	11	2	YHXAE	morphogenetic neur
80	1	9.1	11	2	YHJFHY	morphogenetic neur
81	1	9.1	11	2	A61365	phyllokinin - Rohd
82	1	9.1	11	2	B26744	megascalikinin -
83	1	9.1	11	2	B60409	kassinin-like pept
84	1	9.1	11	2	C60409	kassinin-like pept
85	1	9.1	11	2	S07203	uperolein - frog (
86	1	9.1	11	2	S07207	Crinia-angiotensin
87	1	9.1	11	2	S07201	physalaemin - frog
88	1	9.1	11	2	B58501	24K kidney and bla
89	1	9.1	11	2	D58502	27K bile and gallb
90	1	9.1	11	2	A58502	38K kidney stone p
91	1	9.1	11	2	C58501	42K bile stone pro
92	1	9.1	11	2	F58501	43.5K bile stone p
93	1	9.1	11	2	S58244	pyrroloquinoline q
94	1	9.1	11	2	S04875	nifS protein - Bra
95	1	9.1	11	2	I41138	acetyl ornithine d
96	1	9.1	11	2	S35490	type II site-speci
97	1	9.1	11	2	S21127	precorrin methyltr
98	1	9.1	11	2	S70720	trigger factor hom
99	1	9.1	11	2	S33782	acetolactate synth
100	1	9.1	11	2	B39853	LuxC protein - Pho

#### ALIGNMENTS

##### RESULT 1

S23308

substance P - rainbow trout

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 1 KPR 3

RESULT 2

S23306

substance P - Atlantic cod

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23306

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 1 KPR 3

RESULT 3

S66606

quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)

C;Species: Comamonas testosteroni

C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C;Accession: S66606

R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.

Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66606

A;Molecule type: protein  
A;Residues: 1-11 <SCH>  
A;Experimental source: strain 63

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 9 KPR 11

RESULT 4

S33300

probable substance P - smaller spotted catshark

C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Mar-1999

C;Accession: S33300

R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A;Title: Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, Scyliorhinus canicula.

A;Reference number: S33300; MUID:93292508; PMID:7685693

A;Accession: S33300

A;Molecule type: protein

A;Residues: 1-11 <WAU>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 1 KPR 3

RESULT 5

PH1583

Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1583

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1583  
A;Molecule type: DNA  
A;Residues: 1-11 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 27.3%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARQ 3  
|||  
Db 2 ARQ 4

#### RESULT 6

XASNBA

bradykinin-potentiating peptide B - mamushi

C;Species: Agkistrodon blomhoffi (mamushi)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 08-Dec-1995

C;Accession: A01254

R;Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A;Reference number: A01254

A;Accession: A01254

A;Molecule type: protein

A;Residues: 1-11 <KAT>

A;Note: the sequence of the natural peptide was confirmed by the synthesis and analysis of a peptide having the identical structure and biological properties

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PR 9  
||  
Db 5 PR 6

#### RESULT 7

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence\_revision 23-Oct-1981 #text\_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein

A;Residues: 1-11 <STU>

C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; hormone  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
||  
Db 3 KP 4

RESULT 8

A60654

substance P - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 14-May-1993 #sequence\_revision 27-Jun-1994 #text\_change 08-Dec-1995

C;Accession: A60654

R;Murphy, R.

Neuropeptides 14, 105-110, 1989

A;Title: Primary amino acid sequence of guinea-pig substance P.

A;Reference number: A60654; MUID:90044685; PMID:2478925

A;Accession: A60654

A;Molecule type: protein

A;Residues: 1-11 <MUR>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
||  
Db 3 KP 4

RESULT 9

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 17-Feb-2003

C;Accession: G42762

R;Dick, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.  
Biochemistry 31, 7347-7355, 1992

A;Title: Identification and localization of a cysteinyl residue critical for the  
trypsin-like catalytic activity of the proteasome.

A;Reference number: A42762; MUID:92378961; PMID:1510924

A;Accession: G42762

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <DIC>

A;Note: sequence extracted from NCBI backbone (NCBIP:112176)

C;Superfamily: multicatalytic endopeptidase complex chain C9

C;Keywords: hydrolase



Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QK 4  
||  
Db 7 QK 8

RESULT 10

A33917

dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 07-Nov-1997

C;Accession: A33917

R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.;

Bergh, S.T.; Evans, D.R.

Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989

A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and interdomain linker in the CAD multifunctional polypeptide and properties of the isolated domain.

A;Reference number: A33917; MUID:89282776; PMID:2543974

A;Accession: A33917

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <SIM>

A;Cross-references: GB:M23652

C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Bacillus dihydroorotase homology; biotin carboxylase homology; carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG homology

C;Keywords: hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QK 4  
||  
Db 4 QK 5

RESULT 11

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023

A;Molecule type: protein

A;Residues: 1-11 <CON>

C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; tachykinin  
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 2 PR 3

RESULT 12

S32575

ribosomal protein S2, plastid - squawroot plastid (fragment)

C;Species: *Conopholis americana* (squawroot)

C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 13-Aug-1999

C;Accession: S32575

R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.  
Curr. Genet. 20, 515-518, 1991

A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of photosynthesis in a lineage of parasitic plants.

A;Reference number: S32575; MUID:92145776; PMID:1723664

A;Accession: S32575

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <TAY>

A;Cross-references: EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276

C;Genetics:

A;Gene: rps2

A;Genome: plastid

C;Superfamily: *Escherichia coli* ribosomal protein S2

C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RR 10  
||  
Db 3 RR 4

RESULT 13

A57458

gene Gax protein - mouse (fragment)

C;Species: *Mus sp.* (mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 15-Oct-1999

C;Accession: A57458

R;Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.  
Mol. Cell. Biol. 15, 4272-4281, 1995

A;Title: Regulation of Gax homeobox gene transcription by a combination of positive factors including myocyte-specific enhancer factor 2.

A;Reference number: A57458; MUID:95349593; PMID:7623821

A;Accession: A57458

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA  
A;Residues: 1-11 <RES>  
A;Cross-references: GB:S79168; NID:g1050991  
C;Genetics:  
A;Gene: Gax  
C;Superfamily: unassigned homeobox proteins; homeobox homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
||  
Db 10 RS 11

RESULT 14

A61033

ranatachykinin A - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000

C;Accession: A61033; JE0426

R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.

Regul. Pept. 42(Suppl.1), S12, 1992

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: A61033

A;Accession: A61033

A;Molecule type: protein

A;Residues: 1-11 <KAN>

R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.

Biochem. Biophys. Res. Commun. 177, 588-595, 1991

A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.

A;Reference number: JE0426; MUID:91254337; PMID:2043143

A;Accession: JE0426

A;Molecule type: protein

A;Residues: 1-11 <KOZ>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
||  
Db 1 KP 2

RESULT 15

D61033

ranatachykinin D - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 18-Aug-2000

C;Accession: D61033; JE0429  
 R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.  
 Regul. Pept. 42(Suppl.1), S12, 1992  
 A;Title: Isolation of four novel tachykinins from frog (*Rana catesbeiana*) brain  
 and intestine.  
 A;Reference number: A61033  
 A;Accession: D61033  
 A;Molecule type: protein  
 A;Residues: 1-11 <KAN>  
 R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.  
 Biochem. Biophys. Res. Commun. 177, 588-595, 1991  
 A;Title: Isolation of four novel tachykinins from frog (*Rana catesbeiana*) brain  
 and intestine.  
 A;Reference number: JE0426; MUID:91254337; PMID:2043143  
 A;Accession: JE0429  
 A;Molecule type: protein  
 A;Residues: 1-11 <KOZ>  
 C;Superfamily: unassigned animal peptides  
 C;Keywords: amidated carboxyl end; neuropeptide  
 F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
 ||  
 Db 1 KP 2

RESULT 16  
 S42449  
 ant1 protein - phage P7  
 C;Species: phage P7  
 C;Date: 07-Sep-1994 #sequence\_revision 26-May-1995 #text\_change 08-Oct-1999  
 C;Accession: S42449  
 R;Citron, M.; Schuster, H.  
 Cell 62, 591-598, 1990  
 A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.  
 A;Reference number: S42448; MUID:90335968; PMID:1696181  
 A;Accession: S42449  
 A;Status: preliminary; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-11 <CIT>  
 A;Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
 ||  
 Db 1 MK 2

RESULT 17  
 JQ0395

hypothetical protein (nodB 3' region) - Azorhizobium caulinodans  
 N;Alternate names: hypothetical 1.4K protein  
 C;Species: Azorhizobium caulinodans  
 A;Note: host Sesbania rostrata  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 03-Feb-1994  
 C;Accession: JQ0395  
 R;Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.  
 Mol. Gen. Genet. 219, 289-298, 1989  
 A;Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans:  
 nucleotide sequence and plant-inducible expression.  
 A;Reference number: JQ0393; MUID:90136519; PMID:2615763  
 A;Accession: JQ0395  
 A;Molecule type: DNA  
 A;Residues: 1-11 <GOE>  
 A;Cross-references: GB:L18897  
 A;Experimental source: strain ORS571

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 10 AR 11

#### RESULT 18

PQ0231  
 beta-glucosidase (EC 3.2.1.21) - Cellvibrio gilvus (fragment)  
 C;Species: Cellvibrio gilvus  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 07-May-1999  
 C;Accession: PQ0231  
 R;Kashiwagi, Y.; Iijima, C.; Sasaki, T.; Taniguchi, H.  
 Agric. Biol. Chem. 55, 2553-2559, 1991  
 A;Title: Characterization of a beta-glucosidase encoded by a gene from  
 Cellvibrio gilvus.  
 A;Reference number: PQ0231; MUID:92144103; PMID:1368758  
 A;Accession: PQ0231  
 A;Molecule type: protein  
 A;Residues: 1-11 <KAS>  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QK 4  
 ||  
 Db 9 QK 10

#### RESULT 19

S42587  
 celf protein - Escherichia coli (fragment)  
 C;Species: Escherichia coli  
 C;Date: 25-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
 C;Accession: S42587

R;Guzzo, A.; DuBow, M.S.

Mol. Gen. Genet. 242, 455-460, 1994

A;Title: A luxAB transcriptional fusion to the cryptic celF gene of Escherichia coli displays increased luminescence in the presence of nickel.

A;Reference number: S42587; MUID:94166755; PMID:8121401

A;Accession: S42587

A;Molecule type: DNA

A;Residues: 1-11 <GUZ>

C;Genetics:

A;Gene: celF

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 9 PR 10

#### RESULT 20

B43669

hypothetical protein (rhdA 5' region) - Synechococcus sp. (fragment)

C;Species: Synechococcus sp.

C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 30-Sep-1993

C;Accession: B43669

R;Laudenbach, D.E.; Ehrhardt, D.; Green, L.; Grossman, A.

J. Bacteriol. 173, 2751-2760, 1991

A;Title: Isolation and characterization of a sulfur-regulated gene encoding a periplasmically localized protein with sequence similarity to rhodanese.

A;Reference number: A43669; MUID:91210163; PMID:1708376

A;Accession: B43669

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <LAU>

A;Cross-references: GB:M65244

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQ 3  
||  
Db 9 RQ 10

#### RESULT 21

PC2372

58K heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)

C;Species: Bacillus cereus

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C;Accession: PC2372

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation in *Bacillus cereus*.

A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2372

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <MAS>

C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 10 AR 11

#### RESULT 22

B41835

translation elongation factor EF-G homolog - *Bacillus subtilis* (fragment)

C;Species: *Bacillus subtilis*

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Dec-1997

C;Accession: B41835

R;Mitchell, C.; Morris, P.W.; Vary, J.C.

J. Bacteriol. 174, 2474-2477, 1992

A;Title: Identification of proteins phosphorylated by ATP during sporulation of *Bacillus subtilis*.

A;Reference number: A41835; MUID:92210489; PMID:1556067

A;Accession: B41835

A;Molecule type: protein

A;Residues: 1-11 <MIT>

A;Note: this protein is phosphorylated during stationary phase but not during exponential growth

C;Keywords: phosphoprotein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KT 5  
||  
Db 5 KT 6

#### RESULT 23

E41476

probable antigen 5 - *Mycobacterium leprae* (fragment)

C;Species: *Mycobacterium leprae*

C;Date: 10-Apr-1992 #sequence\_revision 10-Apr-1992 #text\_change 18-Jun-1993

C;Accession: E41476

R;Hartskeerl, R.A.; van Rens, R.M.; Stabel, L.F.E.M.; de Wit, M.Y.L.; Klatser, P.R.

Infect. Immun. 58, 2821-2827, 1990

A;Title: Selection and characterization of recombinant clones that produce *Mycobacterium leprae* antigens recognized by antibodies in sera from household contacts of leprosy patients.

A;Reference number: A41476; MUID:90354041; PMID:1696931  
A;Accession: E41476  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-11 <HAR>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 5 PR 6

RESULT 24

S33519

probable secreted protein - *Acholeplasma laidlawii* (fragment)

C;Species: *Acholeplasma laidlawii*

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 22-Oct-1999

C;Accession: S33519

R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.

submitted to the EMBL Data Library, June 1993

A;Description: Sequence regions from *Acholeplasma laidlawii* which restore export of beta-lactamase in *Escherichia coli*.

A;Reference number: S33518

A;Accession: S33519

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <BOY>

A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
||  
Db 1 MK 2

RESULT 25

H54346

pyruvate synthase (EC 1.2.7.1) alpha chain - *Pyrococcus furiosus* (fragment)

C;Species: *Pyrococcus furiosus*

C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-May-2000

C;Accession: H54346

R;Blamey, J.M.; Adams, M.W.

Biochemistry 33, 1000-1007, 1994

A;Title: Characterization of an ancestral type of pyruvate ferredoxin oxidoreductase from the hyperthermophilic bacterium, *Thermotoga maritima*.

A;Reference number: A54346; MUID:94137707; PMID:8305426

A;Accession: H54346

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BLA>

C;Keywords: coenzyme A; oxidoreductase



Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
||  
Db 3 MK 4

RESULT 26

T06383

hypothetical protein - soybean

C;Species: Glycine max (soybean)

C;Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000

C;Accession: T06383

R;Dewey, R.E.; Wilson, R.F.; Novitzky, W.P.; Goode, J.H.

Plant Cell 6, 1495-1507, 1994

A;Title: The AAPT1 gene of soybean complements a cholinephosphotransferase-deficient mutant of yeast.

A;Reference number: Z06169; MUID:95086383; PMID:7994181

A;Accession: T06383

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-11 <DEW>

A;Cross-references: EMBL:U12735; NID:g530086; PIDN:AAA67718.1; PID:g530087

A;Experimental source: strain Dare; seed

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
||  
Db 1 MK 2

RESULT 27

JQ2307

hypothetical 1.5K protein - tomato chloroplast (strain Toko)

C;Species: chloroplast Lycopersicon esculentum (tomato)

C;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 23-Mar-1995

C;Accession: JQ2307

R;Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A;Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).

A;Reference number: JQ2306

A;Accession: JQ2307

A;Molecule type: DNA

A;Residues: 1-11 <KAW>

A;Experimental source: strain Toko

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
||  
Db 1 MK 2

RESULT 28

JQ2317

hypothetical 1.5K protein - potato chloroplast

C;Species: chloroplast *Solanum tuberosum* (potato)

C;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Jan-1996

C;Accession: JQ2317; JQ2312

R;Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A;Title: Chloroplast DNA evolution in potato (*Solanum tuberosum* L.).

A;Reference number: JQ2306

A;Accession: JQ2317

A;Molecule type: DNA

A;Residues: 1-11 <KW1>

A;Experimental source: cv. W553-4

A;Accession: JQ2312

A;Molecule type: DNA

A;Residues: 1-11 <KW2>

A;Experimental source: cv. 150

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
||  
Db 1 MK 2

RESULT 29

S78026

ribosomal protein YmL29, mitochondrial - yeast (*Saccharomyces cerevisiae*)  
(fragment)

C;Species: *Saccharomyces cerevisiae*

C;Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 14-Nov-1997

C;Accession: S78026

R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittmann-Liebold, B.; Nishimura, T.; Isono, K.

Eur. J. Biochem. 245, 449-456, 1997

A;Title: Identification and characterization of the genes for mitochondrial ribosomal proteins of *Saccharomyces cerevisiae*.

A;Reference number: S78018; MUID:97296414; PMID:9151978

A;Accession: S78026

A;Molecule type: protein

A;Residues: 1-11 <KIT>

C;Genetics:

A;Genome: nuclear

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 8 PR 9

RESULT 30

A34135

DNA-binding protein p - Crithidia fasciculata mitochondrion (fragment)

C;Species: mitochondrion Crithidia fasciculata

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 07-Dec-1999

C;Accession: A34135

R;Tittawella, I.

FEBS Lett. 260, 57-61, 1990

A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata.

A;Reference number: A34135

A;Accession: A34135

A;Molecule type: protein

A;Residues: 1-11 <TIT>

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC6

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 7 PR 8

RESULT 31

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)

N;Alternate names: phosphofructokinase; phosphohexokinase

C;Species: Ascaris suum (pig roundworm)

C;Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 28-Apr-1993

C;Accession: A26120

R;Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.

J. Biol. Chem. 262, 32-34, 1987

A;Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequence of the phosphopeptide.

A;Reference number: A26120; MUID:87083467; PMID:3025208

A;Accession: A26120

A;Molecule type: protein

A;Residues: 1-11 <KUL>

C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
||  
Db 4 RS 5

RESULT 32

C37196

bradykinin-potentiating peptide 3 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994

C;Accession: C37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: C37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 5 PR 6

RESULT 33

D37196

bradykinin-potentiating peptide 4 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994

C;Accession: D37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A;Title: Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.

A;Reference number: A37196; MUID:90351557; PMID:2386615

A;Accession: D37196

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CIN>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            8 PR 9  
             ||  
Db            5 PR 6

RESULT 34

PT0302

Ig heavy chain CRD3 region (clone 5-112) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0302

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain  
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0302

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match                    18.2%;   Score 2;   DB 2;   Length 11;  
Best Local Similarity       100.0%;   Pred. No. 2.6e+04;  
Matches       2;   Conservative       0;   Mismatches       0;   Indels       0;   Gaps       0;

Qy            8 PR 9  
             ||  
Db            4 PR 5

RESULT 35

I54193

Rhesus blood group CcEe protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 21-Jul-2000

C;Accession: I54193

R;Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.;  
Colin, Y.

Genomics 19, 68-74, 1994

A;Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe  
antigens and characterization of the promoter region.

A;Reference number: I54193; MUID:94245182; PMID:8188244

A;Accession: I54193

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:S70456; NID:g546795; PIDN:AAD14061.1; PID:g4261761

C;Genetics:

A;Gene: GDB:RHCE

A;Cross-references: GDB:229957; OMIM:111700

A;Map position: 1p36.2-1p34

Query Match                    18.2%;   Score 2;   DB 2;   Length 11;  
Best Local Similarity       100.0%;   Pred. No. 2.6e+04;  
Matches       2;   Conservative       0;   Mismatches       0;   Indels       0;   Gaps       0;

Qy 8 PR 9  
||  
Db 6 PR 7

RESULT 36

S68637

acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Dec-1997 #sequence\_revision 04-Dec-1997 #text\_change 30-Jan-1998

C;Accession: S68637

R;Boschetti, N.; Brodbeck, U.

FEBS Lett. 380, 133-136, 1996

A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of a single glycosylated protein of 22 kDa.

A;Reference number: S68637; MUID:96181683; PMID:8603722

A;Accession: S68637

A;Molecule type: protein

A;Residues: 1-11 <BOS>

A;Experimental source: brain

C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QK 4  
||  
Db 3 QK 4

RESULT 37

D56979

collagen alpha 1(II) chain - bovine (fragment)

N;Alternate names: collagen alpha 3(XI) chain

C;Species: Bos primigenius taurus (cattle)

C;Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 11-Jul-1997

C;Accession: D56979

R;Wu, J.J.; Eyre, D.R.

J. Biol. Chem. 270, 18865-18870, 1995

A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Insights on polymeric assembly.

A;Reference number: A56978; MUID:95370194; PMID:7642541

A;Accession: D56979

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <WUA>

C;Keywords: pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form 3(XI))  
#status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQ 3  
||

Db 4 RQ 5

RESULT 38

A33571

follistatin - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 30-Sep-1993

C;Accession: A33571

R;Gospodarowicz, D.; Lau, K.

Biochem. Biophys. Res. Commun. 165, 292-298, 1989

A;Title: Pituitary follicular cells secrete both vascular endothelial growth factor and follistatin.

A;Reference number: A33571; MUID:90073725; PMID:2590228

A;Accession: A33571

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <GOS>

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQ 3

||

Db 6 RQ 7

RESULT 39

A14454

6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 28-Apr-1993

C;Accession: A14454

R;Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.

Biochem. Soc. Trans. 7, 721-723, 1979

A;Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.

A;Reference number: A14454; MUID:80004524; PMID:157899

A;Accession: A14454

A;Molecule type: protein

A;Residues: 1-11 <FOR>

C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KT 5

||

Db 9 KT 10

RESULT 40

PH1632

Ig H chain V-D-J region (clone B-less 209) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1632  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1632  
A;Molecule type: DNA  
A;Residues: 1-11 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 2 AR 3

RESULT 41

PH1600  
Ig H chain V-D-J region (wild-type clone 310) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1600  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1600  
A;Molecule type: DNA  
A;Residues: 1-11 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 2 AR 3

RESULT 42

PH1584  
Ig H chain V-D-J region (wild-type clone 8) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1584  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993



A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice using a novel quantitative limiting dilution polymerase chain reaction method.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1584

A;Molecule type: DNA

A;Residues: 1-11 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 2 AR 3

#### RESULT 43

PT0214

T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C;Accession: PT0214

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0214

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 3 AR 4

#### RESULT 44

A49037

TcR gamma V-J region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C;Accession: A49037

R;Ezquerra, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.; Coligan, J.E.

Eur. J. Immunol. 22, 491-498, 1992

A;Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T cell receptor.

A;Reference number: A49037; MUID:92164730; PMID:1311262

A;Accession: A49037

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <EZQ>  
A;Cross-references: GB:S90637; NID:g246288; PIDN:AAB21547.1; PID:g246289  
A;Experimental source: dendritic epidermal T-cell lines  
A;Note: sequence extracted from NCBI backbone (NCBIN:90637, NCBIP:90641)

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
||  
Db 6 RS 7

RESULT 45

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse  
(fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.  
submitted to JIPIID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KT 5  
||  
Db 6 KT 7

RESULT 46

I77447

urinary protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

C;Accession: I77447; I77448

R;Held, W.A.; Gallagher, J.F.; Hohman, C.M.; Kuhn, N.J.; Sampsell, B.M.; Hughes,  
R.G.

Mol. Cell. Biol. 7, 3705-3712, 1987

A;Title: Identification and characterization of functional genes encoding the  
mouse major urinary proteins.

A;Reference number: I57627; MUID:88065510; PMID:2824995

A;Accession: I77447

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>  
A;Cross-references: GB:M17815; NID:g202301; PIDN:AAA40541.1; PID:g202302  
A;Accession: I77448  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <RE2>  
A;Cross-references: GB:M17816; NID:g202303; PIDN:AAA40542.1; PID:g202304

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MK 7  
||  
Db 1 MK 2

RESULT 47

PH0939

T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0939

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental  
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0939

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KP 8  
||  
Db 5 KP 6

RESULT 48

PH0947

T-cell receptor beta chain V-D-J region (clone A2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0947

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental  
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0947

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered from experimentally induced allergic encephalomyelitis  
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RR 10  
||  
Db 4 RR 5

RESULT 49

PH0919

T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0919

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0919

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

A;Note: the authors translated the codon CAG for residue 11 as Glu

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RR 10  
||  
Db 6 RR 7

RESULT 50

T12264

cytochrome-c oxidase (EC 1.9.3.1) chain I - Laudakia caucasia mitochondrion (fragment)

C;Species: mitochondrion Laudakia caucasia

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Aug-2001

C;Accession: T12264; T12267; T12270; T12273; T12276; T12279

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the Laudakia caucasia species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12264

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC1>  
 A;Cross-references: EMBL:AF028681; NID:g3641460; PIDN:AAC99596.1; PID:g3641463  
 A;Experimental source: specimen voucher CAS185010; California Academy of Sciences, San Francisco  
 A;Accession: T12267  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-11 <MAC2>  
 A;Cross-references: EMBL:AF028682; NID:g3641464; PIDN:AAC99599.1; PID:g3641467  
 A;Accession: T12270  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-11 <MAC3>  
 A;Cross-references: EMBL:AF028683; NID:g3641468; PIDN:AAC99602.1; PID:g3641471  
 A;Accession: T12273  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-11 <MAC4>  
 A;Cross-references: EMBL:AF028684; NID:g3641472; PIDN:AAC99605.1; PID:g3641475  
 A;Accession: T12276  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-11 <MAC5>  
 A;Cross-references: EMBL:AF028686; NID:g3641480; PIDN:AAC99611.1; PID:g3641483  
 A;Accession: T12279  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-11 <MAC6>  
 A;Cross-references: EMBL:AF028687; NID:g3641484; PIDN:AAC99614.1; PID:g3641487  
 C;Genetics:  
 A;Gene: COI  
 A;Genome: mitochondrion  
 C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

# RESULT 51

T12253  
 cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia erythrogastra* mitochondrion (fragment)  
 C;Species: mitochondrion *Laudakia erythrogastra*  
 C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Aug-2001  
 C;Accession: T12253; T12257  
 R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.  
 Mol. Phylogenet. Evol. 10, 118-131, 1998  
 A;Title: Phylogenetic relationships among agamid lizards of the *Laudakia caucasia* species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.  
 A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12253  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <MAC1>  
A;Cross-references: EMBL:AF028679; NID:g3641452; PIDN:AAC99590.1; PID:g3641455  
A;Experimental source: specimen voucher CAS182954; California Academy of Sciences, San Francisco  
A;Accession: T12257  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <MAC2>  
A;Cross-references: EMBL:AF028680; NID:g3641456; PIDN:AAC99593.1; PID:g3641459  
A;Experimental source: specimen voucher CAS184400; California Academy of Sciences, San Francisco  
C;Genetics:  
A;Gene: COI  
A;Genome: mitochondrion  
C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

#### RESULT 52

T12244

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia lehmanni* mitochondrion (fragment)

C;Species: mitochondrion *Laudakia lehmanni*

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Aug-2001

C;Accession: T12244

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the *Laudakia caucasia* species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12244

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC>

A;Cross-references: EMBL:AF028677; NID:g3641444; PID:g3641447; PIDN:AAC99584.1

A;Experimental source: specimen voucher CAS183009; California Academy of Sciences, San Francisco

C;Genetics:

A;Gene: COI

A;Genome: mitochondrion

C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

RESULT 53

T12248

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Laudakia microlepis* mitochondrion (fragment)

C;Species: mitochondrion *Laudakia microlepis*

C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 03-Aug-2001

C;Accession: T12248

R;Macey, J.R.; Schulte II, J.A.; Ananjeva, N.B.; Larson, A.; Rastegar-Pouyani, N.; Shammakov, S.M.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 118-131, 1998

A;Title: Phylogenetic relationships among agamid lizards of the *Laudakia caucasia* species group: Testing hypotheses of biogeographic fragmentation and an area cladogram for the Iranian Plateau.

A;Reference number: Z17470; MUID:98424476; PMID:9751922

A;Accession: T12248

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC>

A;Cross-references: EMBL:AF028678; NID:g3641448; PID:g3641451; PIDN:AAC99587.1

A;Experimental source: specimen voucher GNM. RE. ex.-P120; Goteborg Natural History Museum Reptilia Exotica, Goteborg, Sweden

C;Genetics:

A;Gene: COI

A;Genome: mitochondrion

C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

RESULT 54

T17078

cytochrome-c oxidase (EC 1.9.3.1) chain I - *Physignathus cocincinus* mitochondrion (fragment)

C;Species: mitochondrion *Physignathus cocincinus*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 22-Oct-1999

C;Accession: T17078

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A;Title: Evolutionary shifts in three major structural features of the mitochondrial genome among iguanian lizards.

A;Reference number: Z18674; MUID:97315309; PMID:9169559

A;Accession: T17078

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <MAC>

A;Cross-references: EMBL:U82690; NID:g3603140; PID:g3603143; PIDN:AAC62296.1  
C;Genetics:  
A;Genome: mitochondrion  
A;Note: COI  
C;Keywords: mitochondrion; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

RESULT 55

S60294

tubulin 2 beta-3 chain - fruit fly (*Drosophila melanogaster*) (fragment)

C;Species: *Drosophila melanogaster*

C;Date: 19-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jun-2002

C;Accession: S60294

R;Chapel, S.; Sobrier, M.L.; Montpied, P.; Micard, D.; Bruhat, A.; Couderc, J.L.; Dastugue, B.

Insect Mol. Biol. 2, 39-48, 1993

A;Title: In *Drosophila* Kc cells 20-OHE induction of the 60C beta-3 tubulin gene expression is a primary transcriptional event.

A;Reference number: S60292; MUID:97242543; PMID:9087542

A;Accession: S60294

A;Molecule type: mRNA

A;Residues: 1-11 <CHA>

A;Cross-references: EMBL:X60393

C;Genetics:

A;Gene: FlyBase:beta-Tub60D

A;Cross-references: FlyBase:FBgn0003888

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
||  
Db 6 RS 7

RESULT 56

I54081

retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 28-Jun-1999

C;Accession: I54081

R;Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.; Wang, Z.Y.; Larsen, C.J.; Berger, R.

Genes Chromosomes Cancer 6, 133-139, 1993

A;Title: Breakpoint clusters of the PML gene in acute promyelocytic leukemia: primary structure of the reciprocal products of the PML-RARA gene in a patient with t(15;17).

A;Reference number: I54081; MUID:93222087; PMID:7682097



A;Accession: I54081  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-11 <DON>  
A;Cross-references: GB:S57794; NID:g299073; PIDN:AAD13888.1; PID:g4261588  
A;Note: the translation is from an incorrect reading frame  
C;Genetics:  
A;Gene: GDB:RARA  
A;Cross-references: GDB:120337; OMIM:180240  
A;Map position: 17q12-17q12

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.6e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 4 PR 5

RESULT 57

XAVIBH

bradykinin-potentiating peptide - halys viper

N;Alternate names: BPP

C;Species: Agkistrodon halys (halys viper)

C;Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 05-Aug-1994

C;Accession: JC0002

R;Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.

Peptides 6, 339-342, 1985

A;Title: Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys Pallas).

A;Reference number: JC0002; MUID:86177022; PMID:3008123

A;Accession: JC0002

A;Molecule type: protein

A;Residues: 1-11 <CHI>

C;Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin, it is an antihypertensive agent.

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyroglutamic acid; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

RESULT 58

ECLQ2M

tachykinin II - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 08-Dec-1995

C;Accession: S08266  
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.  
FEBS Lett. 261, 397-401, 1990  
A;Title: Locustatachykinin I and II, two novel insect neuropeptides with  
homology to peptides of the vertebrate tachykinin family.  
A;Reference number: S08265; MUID:90184489; PMID:2311766  
A;Accession: S08266  
A;Molecule type: protein  
A;Residues: 1-11 <SCH>  
C;Superfamily: tachykinin  
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin  
F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 1 A 1

RESULT 59

EOOCC

eledoisin - curled octopus

C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 20-Mar-1998

C;Accession: B01561; A01561

R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active  
endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: B01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;  
secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

RESULT 60

EOOC

eledoisin - musky octopus

C;Species: Eledone moschata, Ozaena moschata (musky octopus)

C;Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998

C;Accession: A01561

R;Anastasi, A.; Erspamer, V.  
Arch. Biochem. Biophys. 101, 56-65, 1963  
A;Title: The isolation and amino acid sequence of eledoisin, the active  
endecapeptide of the posterior salivary glands of Eledone.  
A;Reference number: A01561  
A;Accession: A01561  
A;Molecule type: protein  
A;Residues: 1-11 <ANA>  
C;Superfamily: substance P precursor  
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;  
secretagogue; vasodilator; venom  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

RESULT 61

GMROL

leucosulfakinin - Madeira cockroach

N;Alternate names: LSK

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 13-Sep-1996

C;Accession: A01622

R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.

Science 234, 71-73, 1986

A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to  
gastrin and cholecystokinin.

A;Reference number: A01622; MUID:86315858; PMID:3749893

A;Accession: A01622

A;Molecule type: protein

A;Residues: 1-11 <NAC>

C;Superfamily: gastrin

C;Keywords: amidated carboxyl end; hormone; sulfoprotein

F;6/Binding site: sulfate (Tyr) (covalent) #status experimental

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 2 Q 2

RESULT 62

LFTWWE

probable trpEG leader peptide - Thermus aquaticus

C;Species: Thermus aquaticus

C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 16-Jul-1999

C;Accession: S03315  
 R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.  
 Biochim. Biophys. Acta 950, 303-312, 1988  
 A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and trpG.  
 A;Reference number: S03315; MUID:89000781; PMID:2844259  
 A;Accession: S03315  
 A;Molecule type: DNA  
 A;Residues: 1-11 <SAT>  
 A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565.1; PID:g48262  
 A;Note: the source is designated as *Thermus thermophilus* HB8  
 C;Genetics:  
 A;Gene: trpL  
 C;Superfamily: probable trpEG leader peptide

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 M 6  
 |  
 Db 1 M 1

#### RESULT 63

S66196  
 alcohol dehydrogenase (EC 1.1.1.1) class III high affinity form - cod (*Gadus* sp.) (fragment)  
 C;Species: *Gadus* sp. (cod)  
 C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 12-Jun-1998  
 C;Accession: S66196  
 R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.; Michel, H.; Shabanowitz, J.; Hunt, D.F.; Joernvall, H. FEBS Lett. 367, 237-240, 1995  
 A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. Mass-spectrometric analysis of plant, lower vertebrate and higher vertebrate class I, II, and III forms of the enzyme.  
 A;Reference number: S66191; MUID:95331382; PMID:7607314  
 A;Accession: S66196  
 A;Molecule type: protein  
 A;Residues: 1-11 <HJE>  
 C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
 C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 T 5  
 |  
 Db 1 T 1

#### RESULT 64

S68392  
 H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - *Chlamydomonas reinhardtii* chloroplast (fragment)

N;Alternate names: ATP synthase chain I  
 C;Species: chloroplast Chlamydomonas reinhardtii  
 C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 03-Jun-2002  
 C;Accession: S68392  
 R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.  
 FEBS Lett. 377, 163-166, 1995  
 A;Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal amino acid sequences of the CF(0)CF(1) subunits.  
 A;Reference number: S68388; MUID:96128220; PMID:8543042  
 A;Accession: S68392  
 A;Molecule type: protein  
 A;Residues: 1-11 <FIE>  
 A;Experimental source: strain CW15  
 C;Genetics:  
 A;Genome: chloroplast  
 C;Superfamily: H<sup>+</sup>-transporting ATP synthase protein 6  
 C;Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 6 Q 6

#### RESULT 65

B49164  
 chromogranin-B - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 31-Oct-1997  
 C;Accession: B49164  
 R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.  
 Endocrinology 129, 3147-3156, 1991  
 A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides through processing at mono-, di-, or tribasic residues.  
 A;Reference number: A49164; MUID:92063871; PMID:1954895  
 A;Accession: B49164  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-11 <NIE>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:66370)  
 C;Superfamily: chromogranin B precursor

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 P 8  
 |  
 Db 1 P 1

#### RESULT 66

A40693

transgelin - sheep (fragment)  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 31-Oct-1997  
 C;Accession: A40693  
 R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.  
 J. Cell Biol. 121, 1065-1073, 1993  
 A;Title: Purification and properties of transgelin: a transformation and shape change sensitive actin-gelling protein.  
 A;Reference number: A40693; MUID:93273790; PMID:8501116  
 A;Accession: A40693  
 A;Molecule type: protein  
 A;Residues: 1-11 <SHA>  
 A;Experimental source: aorta  
 C;Comment: This protein gels actin and is down regulated by transformation or loss of cell adherence in culture.  
 C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein SM22 homology  
 C;Keywords: actin binding; cytoskeleton

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 K 4  
 |  
 Db 1 K 1

#### RESULT 67

A38841  
 rhodopsin homolog - squid (Watasenia scintillans) (fragment)  
 N;Alternate names: visual pigment protein  
 C;Species: Watasenia scintillans (sparkling enope)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 31-Oct-1997  
 C;Accession: A38841  
 R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.  
 Biochim. Biophys. Acta 957, 318-321, 1988  
 A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.  
 A;Reference number: PT0063; MUID:89051045; PMID:3191148  
 A;Accession: A38841  
 A;Molecule type: protein  
 A;Residues: 1-11 <SEI>  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: chromoprotein; retinal  
 F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 2 A 2

#### RESULT 68

PQ0682

photosystem I 17.5K D2 chain - common tobacco (fragment)

C;Species: *Nicotiana tabacum* (common tobacco)

C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999

C;Accession: PQ0682

R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiura, M.

Plant Physiol. 102, 1259-1267, 1993

A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are all present in isoforms in *Nicotiana* spp.

A;Reference number: PQ0667; MUID:94105345; PMID:8278548

A;Accession: PQ0682

A;Molecule type: protein

A;Residues: 1-11 <OBO>

C;Superfamily: photosystem I chain II

C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1

|

Db 1 A 1

RESULT 69

S00616

parasporal crystal protein, wax moth-specific - *Bacillus thuringiensis* (strain galleriae 11-67) (fragment)

N;Alternate names: delta-endotoxin; parasporal crystal protein positive chain

C;Species: *Bacillus thuringiensis*

C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 13-Sep-1996

C;Accession: S00616

R;Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.

FEBS Lett. 232, 249-251, 1988

A;Title: *Bacillus thuringiensis* ssp. galleriae simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity.

A;Reference number: S00615

A;Accession: S00616

A;Molecule type: protein

A;Residues: 1-11 <CHE>

C;Comment: This toxin is effective against the larvae of *Galleria melonella* (greater wax moth) but not those of *Lymantria dispar* (gypsy moth).

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 P 8

|

Db 2 P 2

RESULT 70

C53652

rhlR protein - *Pseudomonas aeruginosa* (fragment)

C;Species: *Pseudomonas aeruginosa*

C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Aug-1998

C;Accession: C53652

R;Ochsner, U.A.; Fiechter, A.; Reiser, J.

J. Biol. Chem. 269, 19787-19795, 1994

A;Title: Isolation, characterization, and expression in *Escherichia coli* of the *Pseudomonas aeruginosa* rhlAB genes encoding a rhamnosyltransferase involved in rhamnolipid biosurfactant synthesis.

A;Reference number: A53652; MUID:94327521; PMID:8051059

A;Accession: C53652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-11 <OCH>

A;Cross-references: GB:L28170

C;Superfamily: sdiA regulatory protein

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 M 6  
|  
Db 1 M 1

#### RESULT 71

S09074

cytochrome P450-4b - rat (fragment)

N;Alternate names: cytochrome P450K-5

N;Contains: oxidoreductase (EC 1.-.-.-)

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 23-Apr-1993 #sequence\_revision 23-Apr-1993 #text\_change 05-Mar-1999

C;Accession: S09074

R;Imaoka, S.; Terano, Y.; Funae, Y.

Arch. Biochem. Biophys. 278, 168-178, 1990

A;Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with starvation.

A;Reference number: S09072; MUID:90210577; PMID:2321956

A;Accession: S09074

A;Molecule type: protein

A;Residues: 1-11 <IMA>

C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 P 8  
|  
Db 4 P 4

#### RESULT 72



A26930

ermG leader peptide 1 - *Bacillus sphaericus*

C;Species: *Bacillus sphaericus*

C;Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 24-Sep-1999

C;Accession: A26930

R;Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resistance element from *Bacillus sphaericus*.

A;Reference number: A91840; MUID:87083389; PMID:3025178

A;Accession: A26930

A;Molecule type: DNA

A;Residues: 1-11 <MON>

A;Cross-references: GB:M15332; NID:g142881; PIDN:AAA22417.1; PID:g142882

C;Superfamily: unassigned leader peptides

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 M 6

|

Db 1 M 1

RESULT 73

D60409

kassinin-like peptide K-III - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000

C;Accession: D60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;

Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: D60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3

|

Db 1 Q 1

RESULT 74

F60409

substance P-like peptide II - frog (*Pseudophryne guentheri*)

C;Species: Pseudophryne guentheri  
C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000  
C;Accession: F60409  
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;  
Melchiorri, P.; Erspamer, V.  
Peptides 11, 299-304, 1990  
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.  
A;Reference number: A60409; MUID:90287814; PMID:2356157  
A;Accession: F60409  
A;Molecule type: protein  
A;Residues: 1-11 <SIM>  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

RESULT 75

E60409  
substance P-like peptide I - frog (Pseudophryne guentheri)  
C;Species: Pseudophryne guentheri  
C;Date: 30-Jan-1993 #sequence\_revision 30-Jan-1993 #text\_change 02-Sep-2000  
C;Accession: E60409  
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;  
Melchiorri, P.; Erspamer, V.  
Peptides 11, 299-304, 1990  
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of  
the Australian frog Pseudophryne guentheri.  
A;Reference number: A60409; MUID:90287814; PMID:2356157  
A;Accession: E60409  
A;Molecule type: protein  
A;Residues: 1-11 <SIM>  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 9.1%; Score 1; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

Search completed: April 8, 2004, 15:49:26  
Job time : 9.61538 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds  
(without alignments)  
95.432 Million cell updates/sec

Title: US-09-787-443A-12  
Perfect score: 11  
Sequence: 1 ARQKTMKPRRS 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

8

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	4	36.4	11	10	US-09-832-355A-8	Sequence 8, Appli
2	3	27.3	11	8	US-08-801-405B-6	Sequence 6, Appli
3	3	27.3	11	8	US-08-996-470-2	Sequence 2, Appli
4	3	27.3	11	9	US-09-729-402-3	Sequence 3, Appli
5	3	27.3	11	9	US-09-817-310-5	Sequence 5, Appli
6	3	27.3	11	9	US-09-802-109-7	Sequence 7, Appli
7	3	27.3	11	9	US-09-884-681-35	Sequence 35, Appl
8	3	27.3	11	9	US-09-854-204-42	Sequence 42, Appl
9	3	27.3	11	9	US-09-839-743-19	Sequence 19, Appl
10	3	27.3	11	9	US-09-949-196-17	Sequence 17, Appl
11	3	27.3	11	9	US-09-955-504-29	Sequence 29, Appl
12	3	27.3	11	9	US-09-851-138-107	Sequence 107, App
13	3	27.3	11	9	US-09-851-138-108	Sequence 108, App
14	3	27.3	11	9	US-09-367-703-7	Sequence 7, Appli
15	3	27.3	11	10	US-09-983-802-423	Sequence 423, App
16	3	27.3	11	10	US-09-974-879-330	Sequence 330, App
17	3	27.3	11	10	US-09-988-792-6	Sequence 6, Appli
18	3	27.3	11	10	US-09-988-792-9	Sequence 9, Appli
19	3	27.3	11	10	US-09-988-792-10	Sequence 10, Appl
20	3	27.3	11	10	US-09-882-291-45	Sequence 45, Appl
21	3	27.3	11	10	US-09-775-052-4	Sequence 4, Appli
22	3	27.3	11	10	US-09-775-052-40	Sequence 40, Appl
23	3	27.3	11	10	US-09-775-052-55	Sequence 55, Appl
24	3	27.3	11	10	US-09-775-052-56	Sequence 56, Appl
25	3	27.3	11	10	US-09-775-052-57	Sequence 57, Appl
26	3	27.3	11	10	US-09-876-904A-100	Sequence 100, App
27	3	27.3	11	10	US-09-876-904A-157	Sequence 157, App
28	3	27.3	11	10	US-09-876-904A-364	Sequence 364, App
29	3	27.3	11	10	US-09-876-904A-481	Sequence 481, App
30	3	27.3	11	10	US-09-876-904A-610	Sequence 610, App
31	3	27.3	11	10	US-09-922-226-78	Sequence 78, Appl
32	3	27.3	11	10	US-09-892-877-299	Sequence 299, App
33	3	27.3	11	10	US-09-305-736-330	Sequence 330, App
34	3	27.3	11	10	US-09-992-665-6	Sequence 6, Appli
35	3	27.3	11	10	US-09-852-910-75	Sequence 75, Appl
36	3	27.3	11	10	US-09-852-910-228	Sequence 228, App
37	3	27.3	11	10	US-09-948-783-312	Sequence 312, App
38	3	27.3	11	10	US-09-978-309A-25	Sequence 25, Appl
39	3	27.3	11	10	US-09-940-316B-35	Sequence 35, Appl
40	3	27.3	11	10	US-09-940-316B-41	Sequence 41, Appl
41	3	27.3	11	10	US-09-940-316B-53	Sequence 53, Appl
42	3	27.3	11	11	US-09-818-683-330	Sequence 330, App
43	3	27.3	11	12	US-09-784-553C-54	Sequence 54, Appl
44	3	27.3	11	12	US-09-973-278-650	Sequence 650, App
45	3	27.3	11	12	US-10-444-070-15	Sequence 15, Appl
46	3	27.3	11	12	US-10-621-401-330	Sequence 330, App
47	3	27.3	11	12	US-10-620-462-7	Sequence 7, Appli
48	3	27.3	11	13	US-10-146-221-15	Sequence 15, Appl
49	3	27.3	11	13	US-10-125-452-29	Sequence 29, Appl
50	3	27.3	11	14	US-10-180-326-5	Sequence 5, Appli
51	3	27.3	11	14	US-10-003-978A-3	Sequence 3, Appli
52	3	27.3	11	14	US-10-077-555-5	Sequence 5, Appli
53	3	27.3	11	14	US-10-024-535A-6	Sequence 6, Appli
54	3	27.3	11	14	US-10-006-869-3080	Sequence 3080, Ap
55	3	27.3	11	14	US-10-006-869-3125	Sequence 3125, Ap
56	3	27.3	11	14	US-10-006-869-3170	Sequence 3170, Ap

57	3	27.3	11	14	US-10-006-869-3215	Sequence 3215, Ap
58	3	27.3	11	14	US-10-006-869-3260	Sequence 3260, Ap
59	3	27.3	11	14	US-10-229-915-22	Sequence 22, Appl
60	3	27.3	11	14	US-10-192-867-5	Sequence 5, Appli
61	3	27.3	11	14	US-10-211-088-297	Sequence 297, App
62	3	27.3	11	14	US-10-136-738-3	Sequence 3, Appli
63	3	27.3	11	14	US-10-072-602B-502	Sequence 502, App
64	3	27.3	11	14	US-10-230-381-57	Sequence 57, Appl
65	3	27.3	11	14	US-10-231-894-4	Sequence 4, Appli
66	3	27.3	11	14	US-10-286-457-327	Sequence 327, App
67	3	27.3	11	14	US-10-286-457-646	Sequence 646, App
68	3	27.3	11	14	US-10-293-580-35	Sequence 35, Appl
69	3	27.3	11	14	US-10-161-791-290	Sequence 290, App
70	3	27.3	11	14	US-10-405-339-14	Sequence 14, Appl
71	3	27.3	11	14	US-10-231-889-4	Sequence 4, Appli
72	3	27.3	11	15	US-10-285-394-292	Sequence 292, App
73	3	27.3	11	15	US-10-395-032-3080	Sequence 3080, Ap
74	3	27.3	11	15	US-10-395-032-3125	Sequence 3125, Ap
75	3	27.3	11	15	US-10-395-032-3170	Sequence 3170, Ap
76	3	27.3	11	15	US-10-395-032-3215	Sequence 3215, Ap
77	3	27.3	11	15	US-10-395-032-3260	Sequence 3260, Ap
78	3	27.3	11	15	US-10-378-173-207	Sequence 207, App
79	3	27.3	11	15	US-10-378-065-15	Sequence 15, Appl
80	3	27.3	11	15	US-10-394-980-33	Sequence 33, Appl
81	3	27.3	11	15	US-10-361-208-212	Sequence 212, App
82	3	27.3	11	15	US-10-209-201C-54	Sequence 54, Appl
83	3	27.3	11	15	US-10-411-336A-75	Sequence 75, Appl
84	3	27.3	11	15	US-10-411-336A-228	Sequence 228, App
85	2	18.2	11	8	US-08-859-699-10	Sequence 10, Appl
86	2	18.2	11	8	US-08-450-842-45	Sequence 45, Appl
87	2	18.2	11	8	US-08-424-550B-402	Sequence 402, App
88	2	18.2	11	8	US-08-424-550B-476	Sequence 476, App
89	2	18.2	11	8	US-08-424-550B-523	Sequence 523, App
90	2	18.2	11	8	US-08-809-423A-5	Sequence 5, Appli
91	2	18.2	11	8	US-08-817-832B-30	Sequence 30, Appl
92	2	18.2	11	8	US-08-765-837-15	Sequence 15, Appl
93	2	18.2	11	8	US-08-344-824-28	Sequence 28, Appl
94	2	18.2	11	9	US-09-222-179-1	Sequence 1, Appli
95	2	18.2	11	9	US-09-113-924-18	Sequence 18, Appl
96	2	18.2	11	9	US-09-726-624-8	Sequence 8, Appli
97	2	18.2	11	9	US-09-802-077-14	Sequence 14, Appl
98	2	18.2	11	9	US-09-802-077-33	Sequence 33, Appl
99	2	18.2	11	9	US-09-802-096-14	Sequence 14, Appl
100	2	18.2	11	9	US-09-802-096-33	Sequence 33, Appl

#### ALIGNMENTS

RESULT 1  
 US-09-832-355A-8  
 ; Sequence 8, Application US/09832355A  
 ; Publication No. US20030027751A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kovesdi, Imre  
 ; APPLICANT: Kessler, Paul  
 ; TITLE OF INVENTION: VEGF FUSION PROTEINS

; FILE REFERENCE: 205654  
; CURRENT APPLICATION NUMBER: US/09/832,355A  
; CURRENT FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-832-355A-8

Query Match 36.4%; Score 4; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPRR 10  
||||  
Db 8 KPRR 11

RESULT 2

US-08-801-405B-6

; Sequence 6, Application US/08801405B  
; Publication No. US20020019008A1  
; GENERAL INFORMATION:  
; APPLICANT: ROUGEOT, Catherine  
; ROUGEON, Francois  
; TITLE OF INVENTION: THERAPEUTIC USE OF THE SMR1 PROTEIN, THE  
; SMR1 MATURATION PRODUCTS, SPECIFICALLY THE QHNPR  
; PENTAPEPTIDE AS WELL AS ITS BIOLOGICALLY ACTIVE  
; DERIVATIVES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/801,405B  
; FILING DATE: 20-Feb-1997  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dadio, Susan M.  
; REGISTRATION NUMBER: 40,373  
; REFERENCE/DOCKET NUMBER: 012880-003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:

;           LENGTH: 11 amino acids  
;           TYPE: amino acid  
;           STRANDEDNESS: single  
;           TOPOLOGY: linear  
;       MOLECULE TYPE: peptide  
;       SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-08-801-405B-6

Query Match                   27.3%; Score 3; DB 8; Length 11;  
Best Local Similarity   100.0%; Pred. No. 7.8e+03;  
Matches       3; Conservative   0; Mismatches    0; Indels       0; Gaps       0;

Qy           8 PRR 10  
              |||  
Db           4 PRR 6

RESULT 3

US-08-996-470-2

; Sequence 2, Application US/08996470A  
; Publication No. US20020077314A1  
; GENERAL INFORMATION:  
; APPLICANT: Falk  
; TITLE OF INVENTION: Use of Hyaluronic Acid and Forms to Prevent Arterial  
; TITLE OF INVENTION: Restenosis  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/08/996,470A  
; CURRENT FILING DATE: 1997-12-22  
; EARLIER APPLICATION NUMBER: US 07/675,908  
; EARLIER FILING DATE: 1991-07-03  
; EARLIER APPLICATION NUMBER: US 07/838,674  
; EARLIER FILING DATE: 1992-02-21  
; EARLIER APPLICATION NUMBER: US 07/838,675  
; EARLIER FILING DATE: 1992-02-21  
; EARLIER APPLICATION NUMBER: US 08/125,398  
; EARLIER FILING DATE: 1993-09-23  
; EARLIER APPLICATION NUMBER: US 08/285,764  
; EARLIER FILING DATE: 1994-08-03  
; EARLIER APPLICATION NUMBER: US 07/952,095  
; EARLIER FILING DATE: 1992-09-28  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
;   LENGTH: 11  
;   TYPE: PRT  
;   ORGANISM: Artificial Sequence  
;   FEATURE:  
;   NAME/KEY: BINDING  
;   LOCATION: (1)..(11)  
;   OTHER INFORMATION: Scrambled peptide consisting of randomly arranged  
;   OTHER INFORMATION: amino acids 401-411 located in the hyaluronic acid  
;   OTHER INFORMATION: binding region of RHAMM  
US-08-996-470-2

Query Match                   27.3%; Score 3; DB 8; Length 11;  
Best Local Similarity   100.0%; Pred. No. 7.8e+03;  
Matches       3; Conservative   0; Mismatches    0; Indels       0; Gaps       0;

Qy 2 RQK 4  
|||  
Db 1 RQK 3

RESULT 4

US-09-729-402-3

; Sequence 3, Application US/09729402  
; Patent No. US20010021379A1  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; Eberhardt, Christine D.  
; Gray, Patrick W.  
; Le Trong, Hai  
; Tjoelker, Larry W.  
; Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/729,402  
; FILING DATE: 04-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/318,905  
; FILING DATE: 06-OCT-1994  
; APPLICATION NUMBER: US 08/133,803  
; FILING DATE: 06-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20010021379A1and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/32793  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3658  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-729-402-3



Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 1 MKP 3

RESULT 5

US-09-817-310-5

; Sequence 5, Application US/09817310  
; Patent No. US20010042254A1  
; GENERAL INFORMATION:  
; APPLICANT: Stewart, Mary  
; APPLICANT: Kozma, Sarah  
; APPLICANT: Thomas, George  
; TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase  
; FILE REFERENCE: 4-20971/A  
; CURRENT APPLICATION NUMBER: US/09/817,310  
; CURRENT FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 09/230,247  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:mammalian  
; OTHER INFORMATION: autoinhibitory domain  
US-09-817-310-5

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 3 PRR 5

RESULT 6

US-09-802-109-7

; Sequence 7, Application US/09802109  
; Patent No. US20020058611A1  
; GENERAL INFORMATION:  
; APPLICANT: Stein, Stanley  
; TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC  
; FILE REFERENCE: 601-1-083  
; CURRENT APPLICATION NUMBER: US/09/802,109  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: 09/044,411  
; PRIOR FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Same as Sequence ID 2, but with a substitution of
; OTHER INFORMATION: Gln to Pro.
; NAME/KEY: BINDING
; LOCATION: (10)
; OTHER INFORMATION: Cys(biotin)
; OTHER INFORMATION: Peptide has an N-terminal acetyl group.
; OTHER INFORMATION: Peptide has a C-terminal amide group.
US-09-802-109-7
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      8 PRR 10
      |||
Db      6 PRR 8
```

# RESULT 7

US-09-884-681-35

; Sequence 35, Application US/09884681

; Patent No. US20020061546A1

; GENERAL INFORMATION:

; APPLICANT: Tsien, Roger Y.

; Cubitt, Andrew B.

; TITLE OF INVENTION: Assays for Protein Kinases Using  
; Fluorescent Protein Substrates

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/884,681

; FILING DATE: 19-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/679,865

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Storella, John S.

; REGISTRATION NUMBER: 32,944

; REFERENCE/DOCKET NUMBER: 02307Z-069000

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-884-681-35

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      9 RRS 11
        |||
Db      4 RRS 6

```

# RESULT 8

```

US-09-854-204-42
; Sequence 42, Application US/09854204
; Patent No. US20020098236A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Peter Martin
; APPLICANT: Zhelev, Nikolai
; TITLE OF INVENTION: Transport Vectors
; FILE REFERENCE: CCI-010
; CURRENT APPLICATION NUMBER: US/09/854,204
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/438,460
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: GB 9825000.4
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: GB 9825001.2
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: GB 9902525.6
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: GB 9902522.3
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: GB 9914578.1
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: PCT/GB99/03750
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: bAla

```

; NAME/KEY: MOD\_RES  
; LOCATION: (11)  
; OTHER INFORMATION: AMIDATION  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: sequence  
US-09-854-204-42

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 1 ARQ 3

RESULT 9

US-09-839-743-19

; Sequence 19, Application US/09839743  
; Patent No. US20020146824A1  
; GENERAL INFORMATION:  
; APPLICANT: The Salk Institute for Biological Sciences  
; APPLICANT: Lamb, Christopher  
; APPLICANT: Doerner, Peter  
; APPLICANT: Laible, Goetz  
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and  
; TITLE OF INVENTION: Transcription Factor and Methods of Use Thereof  
; FILE REFERENCE: SALKINS.008DV3  
; CURRENT APPLICATION NUMBER: US/09/839,743  
; CURRENT FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: US 09/401,336  
; PRIOR FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: US 09/189,344  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 08/669,721  
; PRIOR FILING DATE: 1996-06-27  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Nicotiana tabacum  
US-09-839-743-19

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 4 KPR 6

RESULT 10

US-09-949-196-17

; Sequence 17, Application US/09949196  
; Patent No. US20020147145A1

```
; GENERAL INFORMATION:
; APPLICANT: Zealand Pharmaceuticals A/S
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF
Cdc25A IN RESPONSE
; TITLE OF INVENTION: TO DNA DAMAGE
; FILE REFERENCE: 55888 (45487)
; CURRENT APPLICATION NUMBER: US/09/949,196
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
sequence
US-09-949-196-17
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 ARQ 3
      |||
Db      6 ARQ 8
```

```
RESULT 11
US-09-955-504-29
; Sequence 29, Application US/09955504
; Publication No. US20020182702A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT006P2
; CURRENT APPLICATION NUMBER: US/09/955,504
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,222
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 09/712,907
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: PCT/US00/14308
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/178,717
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/142,930
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/136,388
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-504-29
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Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 3 PRR 5

RESULT 12

US-09-851-138-107

; Sequence 107, Application US/09851138

; Publication No. US20020183508A1

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT

; STUYVER, LIEVEN

; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND

DIAGNOSTIC

; AGENTS

; NUMBER OF SEQUENCES: 207

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARNOLD, WHITE & DURKEE

; STREET: P.O. BOX 4433

; CITY: HOUSTON

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Microsoft Word 6.0 / ASCII text output

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/851,138

; FILING DATE: 09-May-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/836,075

; FILING DATE: <Unknown>

; APPLICATION NUMBER: EP 94870166.9

; FILING DATE: 21 Oct 1994

; APPLICATION NUMBER: EP 95870076.7

; FILING DATE: 28 Jun 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KAMMERER, PATRICIA A.

; REGISTRATION NUMBER: 29,775

; REFERENCE/DOCKET NUMBER: INNS:004

; INFORMATION FOR SEQ ID NO: 107:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 107:

US-09-851-138-107

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 1 ARQ 3

RESULT 13

US-09-851-138-108

; Sequence 108, Application US/09851138

; Publication No. US20020183508A1

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT

; STUYVER, LIEVEN

; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND

DIAGNOSTIC

; AGENTS

; NUMBER OF SEQUENCES: 207

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARNOLD, WHITE & DURKEE

; STREET: P.O. BOX 4433

; CITY: HOUSTON

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Microsoft Word 6.0 / ASCII text output

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/851,138

; FILING DATE: 09-May-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/836,075

; FILING DATE: <Unknown>

; APPLICATION NUMBER: EP 94870166.9

; FILING DATE: 21 Oct 1994

; APPLICATION NUMBER: EP 95870076.7

; FILING DATE: 28 Jun 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KAMMERER, PATRICIA A.

; REGISTRATION NUMBER: 29,775

; REFERENCE/DOCKET NUMBER: INNS:004

; INFORMATION FOR SEQ ID NO: 108:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 108:

US-09-851-138-108

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 2 RRS 4

RESULT 14

US-09-367-703-7

; Sequence 7, Application US/09367703  
; Publication No. US20020198361A1  
; GENERAL INFORMATION:  
; APPLICANT: ROUGEOT, Catherine  
; APPLICANT: ROUGEON, Francois  
; TITLE OF INVENTION: THERAPEUTIC USE OF THE SMR 1 PROTEIN AND ACTIVE  
; TITLE OF INVENTION: DERIVATIVES THEREOF  
; FILE REFERENCE: 0660-0158-0PCT  
; CURRENT APPLICATION NUMBER: US/09/367,703  
; CURRENT FILING DATE: 1999-10-13  
; PRIOR APPLICATION NUMBER: PCT/EP98/00956  
; PRIOR FILING DATE: 1998-02-19  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-09-367-703-7

Query Match 27.3%; Score 3; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 4 PRR 6

RESULT 15

US-09-983-802-423

; Sequence 423, Application US/09983802  
; Publication No. US20030022185A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer et al.  
; TITLE OF INVENTION: 123 Human Secreted Proteins  
; FILE REFERENCE: PZ010P1  
; CURRENT APPLICATION NUMBER: US/09/983,802  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08



[illegible]

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 423  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-983-802-423

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 5 QKT 7

RESULT 16

US-09-974-879-330

; Sequence 330, Application US/09974879  
; Publication No. US20030028003A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 125 Human Secreted Proteins  
; FILE REFERENCE: PZ020P2  
; CURRENT APPLICATION NUMBER: US/09/974,879  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/239,893  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: US 09/818,683  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 09/305,736  
; PRIOR FILING DATE: 1999-05-05  
; PRIOR APPLICATION NUMBER: PCT/US98/23435  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: US 60/064,911  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,912  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,983  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,900  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,988  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,987  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,908  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,984  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,985  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/066,094

; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: US 60/066,100  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: US 60/066,089  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: US 60/066,095  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: US 60/066,090  
; PRIOR FILING DATE: 1997-11-17  
; NUMBER OF SEQ ID NOS: 611  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 330  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-974-879-330

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 2 RRS 4

RESULT 17

US-09-988-792-6

; Sequence 6, Application US/09988792  
; Publication No. US20030032599A1  
; GENERAL INFORMATION:  
; APPLICANT: Lipkowski, Andrezej W  
; APPLICANT: Carr, Daniel B  
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS  
; FILE REFERENCE: 18475-025  
; CURRENT APPLICATION NUMBER: US/09/988,792  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/252,369  
; PRIOR FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Scyliorhinus canicula  
US-09-988-792-6

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 1 KPR 3

RESULT 18

US-09-988-792-9

; Sequence 9, Application US/09988792  
; Publication No. US20030032599A1  
; GENERAL INFORMATION:  
; APPLICANT: Lipkowski, Andrezej W  
; APPLICANT: Carr, Daniel B  
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS  
; FILE REFERENCE: 18475-025  
; CURRENT APPLICATION NUMBER: US/09/988,792  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/252,369  
; PRIOR FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Gadus morhua

US-09-988-792-9

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 1 KPR 3

RESULT 19

US-09-988-792-10

; Sequence 10, Application US/09988792  
; Publication No. US20030032599A1  
; GENERAL INFORMATION:  
; APPLICANT: Lipkowski, Andrezej W  
; APPLICANT: Carr, Daniel B  
; TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS  
; FILE REFERENCE: 18475-025  
; CURRENT APPLICATION NUMBER: US/09/988,792  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/252,369  
; PRIOR FILING DATE: 2000-11-21  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Oncorhynchus mykiss

US-09-988-792-10

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 1 KPR 3

RESULT 20

US-09-882-291-45

; Sequence 45, Application US/09882291  
 ; Publication No. US20030040472A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zealand Pharmaceuticals A/S  
 ; TITLE OF INVENTION: No. US20030040472A1el Peptide Conjugates  
 ; FILE REFERENCE: 007-2001  
 ; CURRENT APPLICATION NUMBER: US/09/882,291  
 ; CURRENT FILING DATE: 2001-06-15  
 ; NUMBER OF SEQ ID NOS: 77  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 45  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide  
 sequence  
 US-09-882-291-45

Query Match 27.3%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
 |||  
 Db 6 ARQ 8

RESULT 21

US-09-775-052-4

; Sequence 4, Application US/09775052  
 ; Publication No. US20030054000A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dowdy, Steven F.  
 ; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
 ; FILE REFERENCE: 48881/1742  
 ; CURRENT APPLICATION NUMBER: US/09/775,052  
 ; CURRENT FILING DATE: 2001-02-01  
 ; PRIOR APPLICATION NUMBER: 09/208,966  
 ; PRIOR FILING DATE: 1998-12-10  
 ; PRIOR APPLICATION NUMBER: 60/082,402  
 ; PRIOR FILING DATE: 1998-04-20  
 ; PRIOR APPLICATION NUMBER: 60/069,012  
 ; PRIOR FILING DATE: 1997-12-10  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: human  
 US-09-775-052-4

Query Match 27.3%; Score 3; DB 10; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 6 ARQ 8

RESULT 22

US-09-775-052-40

; Sequence 40, Application US/09775052  
; Publication No. US20030054000A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 40  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-40

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 6 ARQ 8

RESULT 23

US-09-775-052-55

; Sequence 55, Application US/09775052  
; Publication No. US20030054000A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10

; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-55

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 8 PRR 10

RESULT 24

US-09-775-052-56

; Sequence 56, Application US/09775052  
; Publication No. US20030054000A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF  
; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 56  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-56

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 5 PRR 7

RESULT 25

US-09-775-052-57

; Sequence 57, Application US/09775052  
; Publication No. US20030054000A1  
; GENERAL INFORMATION:  
; APPLICANT: Dowdy, Steven F.  
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF

; FILE REFERENCE: 48881/1742  
; CURRENT APPLICATION NUMBER: US/09/775,052  
; CURRENT FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 09/208,966  
; PRIOR FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: 60/082,402  
; PRIOR FILING DATE: 1998-04-20  
; PRIOR APPLICATION NUMBER: 60/069,012  
; PRIOR FILING DATE: 1997-12-10  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: human  
US-09-775-052-57

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 5 PRR 7

RESULT 26

US-09-876-904A-100  
; Sequence 100, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 100  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
"Tripartite" or  
; OTHER INFORMATION: "doubly bipartite" NLS of adenovirus DNA polymerase  
US-09-876-904A-100

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 8 PRR 10  
|||  
Db 2 PRR 4

RESULT 27

US-09-876-904A-157

; Sequence 157, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 157  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
; FEATURE:  
; OTHER INFORMATION: Karyophilic peptide  
US-09-876-904A-157

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 7 RRS 9

RESULT 28

US-09-876-904A-364

; Sequence 364, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 364  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human TCF-1  
US-09-876-904A-364

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 5 RRS 7

RESULT 29

US-09-876-904A-481  
; Sequence 481, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 481  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Mouse LFB3.  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(8)  
; OTHER INFORMATION: Any Amino acid  
US-09-876-904A-481

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQK 4  
|||  
Db 9 RQK 11

RESULT 30

US-09-876-904A-610

; Sequence 610, Application US/09876904A  
 ; Publication No. US20030072794A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BOULIKAS, TENI  
 ; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND  
 THERAPEUTIC  
 ; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC  
 PEPTIDE  
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
 ; FILE REFERENCE: TB-2002.00  
 ; CURRENT APPLICATION NUMBER: US/09/876,904A  
 ; CURRENT FILING DATE: 2001-06-08  
 ; PRIOR APPLICATION NUMBER: US 60/210,925  
 ; PRIOR FILING DATE: 2000-06-09  
 ; NUMBER OF SEQ ID NOS: 629  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 610  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Bos sp.  
 ; FEATURE:  
 ; OTHER INFORMATION: Calf Thymus HMG17 (89aa; 9,248 D).  
 US-09-876-904A-610

Query Match 27.3%; Score 3; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
 Db 5 RRS 7

RESULT 31

US-09-922-226-78

; Sequence 78, Application US/09922226  
 ; Publication No. US20030077664A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhao, Yi  
 ; APPLICANT: Thatcher, Scott M.  
 ; APPLICANT: Xiao, Jia-Hao  
 ; APPLICANT: Kusari, Jyotirmoy  
 ; APPLICANT: Chandraratna, Roshantha A.  
 ; TITLE OF INVENTION: Methods of Screening For Compounds That  
 ; TITLE OF INVENTION: Modulate Hormone Receptor Activity  
 ; FILE REFERENCE: P-AR 4681  
 ; CURRENT APPLICATION NUMBER: US/09/922,226  
 ; CURRENT FILING DATE: 2002-01-09  
 ; PRIOR APPLICATION NUMBER: US 60/284,797  
 ; PRIOR FILING DATE: 2001-04-18  
 ; NUMBER OF SEQ ID NOS: 191  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 78  
 ; LENGTH: 11

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-09-922-226-78

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 4 RRS 6

RESULT 32

US-09-892-877-299

; Sequence 299, Application US/09892877  
; Publication No. US20030077809A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 97 Human secreted proteins  
; FILE REFERENCE: PZ028P1  
; CURRENT APPLICATION NUMBER: US/09/892,877  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 299  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-892-877-299

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 1 RRS 3

RESULT 33

US-09-305-736-330

; Sequence 330, Application US/09305736  
; Publication No. US20030088078A1  
; GENERAL INFORMATION:  
; APPLICANT: Feng et al.  
; TITLE OF INVENTION: 125 Human Secreted Proteins  
; FILE REFERENCE: PZ020P1  
; CURRENT APPLICATION NUMBER: US/09/305,736  
; CURRENT FILING DATE: 1999-05-05  
; EARLIER APPLICATION NUMBER: PCT/US98/23435  
; EARLIER FILING DATE: 1998-11-04  
; EARLIER APPLICATION NUMBER: 60/064,911

```

; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,912
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,983
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,900
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,988
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,987
; EARLIER FILING DATE:1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,908
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,984
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,985
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/066,094
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,100
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,089
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60.066,095
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 330
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-305-736-330

```

```

Query Match          27.3%;  Score 3;  DB 10;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 7.8e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      9 RRS 11
        |||
Db      2 RRS 4

```

#### RESULT 34

US-09-992-665-6

```

; Sequence 6, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16

```

; NUMBER OF SEQ ID NOS: 380  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-09-992-665-6

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 9 MKP 11

RESULT 35  
US-09-852-910-75  
; Sequence 75, Application US/09852910  
; Publication No. US20030096297A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamm, Heidi  
; APPLICANT: Gilchrist, Annette  
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled  
Receptor Signaling  
; FILE REFERENCE: 2661-101  
; CURRENT APPLICATION NUMBER: US/09/852,910  
; CURRENT FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US 60/275,472  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 271  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 75  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-852-910-75

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 5 RRS 7

RESULT 36  
US-09-852-910-228  
; Sequence 228, Application US/09852910  
; Publication No. US20030096297A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamm, Heidi  
; APPLICANT: Gilchrist, Annette

```

; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled
Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 228
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: G12 library peptide
US-09-852-910-228

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 TMK 7
        |||
Db      4 TMK 6

```

# RESULT 37

```

US-09-948-783-312
; Sequence 312, Application US/09948783
; Publication No. US20030100051A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: PZ028P2
; CURRENT APPLICATION NUMBER: US/09/948,783
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/231,846
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: 09/892,877
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/437,658
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/09847
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/085,093
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,094
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,105
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,180
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085,927
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,906

```

```

; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,924
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,928
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,920
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 465
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 312
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-948-783-312

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          9 RRS 11
            |||
Db          1 RRS 3

```

# RESULT 38

US-09-978-309A-25

```

; Sequence 25, Application US/09978309A
; Publication No. US20030100490A1
; GENERAL INFORMATION:
; APPLICANT: Cruz, Tony
; APPLICANT: Pastrak, Aleksandra
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response
to
; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated
by
; TITLE OF INVENTION: Hyaladherin and Hyaluronans
; FILE REFERENCE: 033352-010
; CURRENT APPLICATION NUMBER: US/09/978,309A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 09/685,010
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/541,522
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25

```



; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Scrambled hyalauron binding peptide  
US-09-978-309A-25

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQK 4  
|||  
Db 1 RQK 3

RESULT 39

US-09-940-316B-35

; Sequence 35, Application US/09940316B  
; Publication No. US20030175901A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSAN BIOSCIENCES, Inc.  
; APPLICANT: REEVES, CHRISTOPHER  
; APPLICANT: CHU, DANIEL  
; APPLICANT: KHOSLA, CHAITAN  
; APPLICANT: SANTI, DANIEL  
; APPLICANT: WU, KAI  
; TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520  
POLYKETIDE SYNTHASE  
; TITLE OF INVENTION: GENE CLUSTER  
; FILE REFERENCE: 30062-20026.11  
; CURRENT APPLICATION NUMBER: US/09/940,316B  
; CURRENT FILING DATE: 2001-08-27  
; PRIOR APPLICATION NUMBER: 09/410,551  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: US 60/139,650  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: US 60/123,810  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/102,748  
; PRIOR FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS  
; OTHER INFORMATION: synthase fragment  
US-09-940-316B-35

Query Match 27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10

Db                    |||  
                      3 PRR 5

RESULT 40

US-09-940-316B-41

; Sequence 41, Application US/09940316B  
; Publication No. US20030175901A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSAN BIOSCIENCES, Inc.  
; APPLICANT: REEVES, CHRISTOPHER  
; APPLICANT: CHU, DANIEL  
; APPLICANT: KHOSLA, CHAITAN  
; APPLICANT: SANTI, DANIEL  
; APPLICANT: WU, KAI  
; TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520  
POLYKETIDE SYNTHASE  
; TITLE OF INVENTION: GENE CLUSTER  
; FILE REFERENCE: 30062-20026.11  
; CURRENT APPLICATION NUMBER: US/09/940,316B  
; CURRENT FILING DATE: 2001-08-27  
; PRIOR APPLICATION NUMBER: 09/410,551  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: US 60/139,650  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: US 60/123,810  
; PRIOR FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: US 60/102,748  
; PRIOR FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS  
; OTHER INFORMATION: synthase fragment  
US-09-940-316B-41

Query Match                    27.3%; Score 3; DB 10; Length 11;  
Best Local Similarity        100.0%; Pred. No. 7.8e+03;  
Matches        3; Conservative    0; Mismatches    0; Indels        0; Gaps        0;

Qy                    8 PRR 10  
                      |||  
Db                    3 PRR 5

RESULT 41

US-09-940-316B-53

; Sequence 53, Application US/09940316B  
; Publication No. US20030175901A1  
; GENERAL INFORMATION:  
; APPLICANT: KOSAN BIOSCIENCES, Inc.  
; APPLICANT: REEVES, CHRISTOPHER  
; APPLICANT: CHU, DANIEL

```

; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520
POLYKETIDE SYNTHASE
; TITLE OF INVENTION: GENE CLUSTER
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 09/410,551
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-940-316B-53

```

```

Query Match          27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 PRR 10
        |||
Db      3 PRR 5

```

```

RESULT 42
US-09-818-683-330
; Sequence 330, Application US/09818683
; Publication No. US20030211472A1
; GENERAL INFORMATION:
; APPLICANT: Feng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: PZ020P1
; CURRENT APPLICATION NUMBER: US/09/818,683
; CURRENT FILING DATE: 2001-03-28
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 330
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-818-683-330

```

```

Query Match          27.3%; Score 3; DB 11; Length 11;

```

Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 2 RRS 4

RESULT 43

US-09-784-553C-54  
; Sequence 54, Application US/09784553C  
; Publication No. US20040043378A1  
; GENERAL INFORMATION:  
; APPLICANT: ZHOU, MING-MING  
; APPLICANT: AGGARWAL, ANEEL  
; TITLE OF INVENTION: METHODS OF IDENTIFYING MODULATORS OF BROMODOMAINS  
; FILE REFERENCE: 2459-1-003 CIP  
; CURRENT APPLICATION NUMBER: US/09/784,553C  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR APPLICATION NUMBER: 09/510,314  
; PRIOR FILING DATE: 2000-02-22  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 54  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic HIV-1 Tat peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)..(5)  
; OTHER INFORMATION: acetylated lysine  
US-09-784-553C-54

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 7 ARQ 9

RESULT 44

US-09-973-278-650  
; Sequence 650, Application US/09973278  
; Publication No. US20040044191A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer et al.  
; TITLE OF INVENTION: 123 Human Secreted Proteins  
; FILE REFERENCE: PZ010P2  
; CURRENT APPLICATION NUMBER: US/09/973,278  
; CURRENT FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: 60/239,899  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 09/227,357

; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: PCT/US98/13684  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/051,926  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/052,793  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,925  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,929  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/052,803  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/052,732  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,931  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,932  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,916  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,930  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,918  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,920  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/052,733  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/052,795  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,919  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/051,928  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: 60/055,722  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,723  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,948  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,949  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,953  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,950  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,947  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,964  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/056,360  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,684  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,984  
; PRIOR FILING DATE: 1997-08-18

; PRIOR APPLICATION NUMBER: 60/055,954  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/058,785  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: 60/058,664  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: 60/058,660  
; PRIOR FILING DATE: 1997-09-12  
; PRIOR APPLICATION NUMBER: 60/058,661  
; PRIOR FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 947  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 650  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-973-278-650

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 5 QKT 7

RESULT 45

US-10-444-070-15

; Sequence 15, Application US/10444070  
; Publication No. US20040029809A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: SPHERON COMPONENTS USEFUL IN DETERMINING COMPOUNDS  
; TITLE OF INVENTION: CAPABLE OF TREATING SYMPTOMS OF ALZHEIMER'S DISEASE,  
; TITLE OF INVENTION: AND TREATMENTS AND ANIMAL MODELS PRODUCED THEREFROM  
; FILE REFERENCE: 59003.000021  
; CURRENT APPLICATION NUMBER: US/10/444,070  
; CURRENT FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: 10/378,065  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: 60/361,302  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-444-070-15

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
Db 1 RRS 3

RESULT 46

US-10-621-401-330

; Sequence 330, Application US/10621401  
; Publication No. US20040038277A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 125 Human Secreted Proteins  
; FILE REFERENCE: PZ020P2C1  
; CURRENT APPLICATION NUMBER: US/10/621,401  
; CURRENT FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: US 09/974,879  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/239,893  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: US 09/818,683  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 09/305,736  
; PRIOR FILING DATE: 1999-05-05  
; PRIOR APPLICATION NUMBER: PCT/US98/23435  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: US 60/064,911  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,912  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,983  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,900  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,988  
; PRIOR FILING DATE: 1997-11-07  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 611  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 330  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-621-401-330

Query Match 27.3%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
 |||  
Db 2 RRS 4

RESULT 47

US-10-620-462-7

; Sequence 7, Application US/10620462

```

; Publication No. US20040047805A1
; GENERAL INFORMATION:
; APPLICANT: ROUGEOT, Catherine
; APPLICANT: ROUGEOT, Francois
; TITLE OF INVENTION: THERAPEUTIC USE OF THE SMR1 PROTEIN AND ACTIVE
DERIVATIVES THEREOF
; FILE REFERENCE: 0660-0158-0PCT
; CURRENT APPLICATION NUMBER: US/10/620,462
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US/09/367,703B
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PCT/EP98/00956
; PRIOR FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-620-462-7

```

```

Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 PRR 10
      |||
Db      4 PRR 6

```

#### RESULT 48

US-10-146-221-15

```

; Sequence 15, Application US/10146221
; Publication No. US20020173006A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Pabo, Carl O.
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Poly Zinc Finger Proteins With Improved Linkers
; FILE REFERENCE: 019496-002510US
; CURRENT APPLICATION NUMBER: US/10/146,221
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US/09/260,629
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:longer flexible
; OTHER INFORMATION: linker for fusion protein 268//NRE containing a
; OTHER INFORMATION: Gly-Gly-Gly-Ser sequence
US-10-146-221-15

```

```

Query Match          27.3%; Score 3; DB 13; Length 11;

```



Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQK 4  
|||  
Db 1 RQK 3

RESULT 49

US-10-125-452-29

; Sequence 29, Application US/10125452  
; Publication No. US20020173640A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: ADAM Polynucleotides, Polypeptides, and Antibodies  
; FILE REFERENCE: PT006P2  
; CURRENT APPLICATION NUMBER: US/10/125,452  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 09/955,504  
; PRIOR FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: 09/712,907  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: PCT/US00/14308  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 60/178,717  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/142,930  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/136,388  
; PRIOR FILING DATE: 1999-05-27  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-125-452-29

Query Match 27.3%; Score 3; DB 13; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 3 PRR 5

RESULT 50

US-10-180-326-5

; Sequence 5, Application US/10180326  
; Publication No. US20030049661A1  
; GENERAL INFORMATION:  
; APPLICANT: Seino, Susumu  
; APPLICANT: Shibasaki, Tadao  
; APPLICANT: Ozaki, No. US20030049661A1uaki  
; TITLE OF INVENTION: Protein Rim2  
; FILE REFERENCE: P21573

; CURRENT APPLICATION NUMBER: US/10/180,326  
; CURRENT FILING DATE: 2002-06-27  
; PRIOR APPLICATION NUMBER: JP 288372/99  
; PRIOR FILING DATE: 1999-10-08<160> 5  
; NUMBER OF SEQ ID NOS:  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-180-326-5

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 8 PRR 10

RESULT 51

US-10-003-978A-3

; Sequence 3, Application US/10003978A  
; Publication No. US20030072747A1  
; GENERAL INFORMATION:  
; APPLICANT: Cousens, Lawrence S.  
; Eberhardt, Christine D.  
; Gray, Patrick W.  
; Le Trong, Hai  
; Tjoelker, Larry W.  
; Wilder, Cheryl L.  
; TITLE OF INVENTION: Platelet-Activating Factor  
; Acetylhydrolase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, Gerstein & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6357  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/003,978A  
; FILING DATE: 23-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/729,402  
; FILING DATE: 04-DEC-2000  
; APPLICATION NUMBER: US 09/577,758  
; FILING DATE: 23-MAY-2000  
; APPLICATION NUMBER: US 09/010,715

```

; FILING DATE: 22-JAN-1998
; APPLICATION NUMBER: US 08/480,658
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030072747Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/37792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-003-978A-3

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 MKP 8
      |||
Db      1 MKP 3

```

```

RESULT 52
US-10-077-555-5
; Sequence 5, Application US/10077555
; Publication No. US20030077289A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Use of Cell-Penetrating Peptides to Generate Antitumor
Immunity
; FILE REFERENCE: P02373US1/10200806
; CURRENT APPLICATION NUMBER: US/10/077,555
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/268,687
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-077-555-5

```

```

Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 6 ARQ 8

RESULT 53

US-10-024-535A-6

; Sequence 6, Application US/10024535A  
; Publication No. US20030078200A1  
; GENERAL INFORMATION:  
; APPLICANT: MARCEL et al.  
; TITLE OF INVENTION: Therapeutic methods and compositions for the treatment  
; TITLE OF INVENTION: of impaired interpersonal and behavioral disorders  
; FILE REFERENCE: P07479US01/BAS  
; CURRENT APPLICATION NUMBER: US/10/024,535A  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: PCT/EP00/06259  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: US/140,563  
; PRIOR FILING DATE: 1999-06-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: This is a peptide sequence that was designed to achieve  
therapeutic  
; OTHER INFORMATION: effects in mammals.  
US-10-024-535A-6

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 4 PRR 6

RESULT 54

US-10-006-869-3080

; Sequence 3080, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3080  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-10-006-869-3080

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 7 QKT 9

RESULT 55

US-10-006-869-3125  
; Sequence 3125, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3125  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-10-006-869-3125

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 7 QKT 9

RESULT 56

US-10-006-869-3170  
; Sequence 3170, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:

```
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3170
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-10-006-869-3170
```

```
Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          3 QKT 5
            |||
Db          7 QKT 9
```

RESULT 57

```
US-10-006-869-3215
; Sequence 3215, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3215
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence
US-10-006-869-3215
```

```
Query Match          27.3%; Score 3; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          3 QKT 5
```

Db                    |||  
                      7 QKT 9

RESULT 58

US-10-006-869-3260  
; Sequence 3260, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3260  
;    LENGTH: 11  
;    TYPE: PRT  
;    ORGANISM: Artificial Sequence  
;    FEATURE:  
;    OTHER INFORMATION: Representative cyclic modulating agent based on  
;    OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-10-006-869-3260

Query Match                    27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity    100.0%; Pred. No. 7.8e+03;  
Matches        3; Conservative        0; Mismatches        0; Indels        0; Gaps        0;

QY                    3 QKT 5  
                      |||  
Db                    7 QKT 9

RESULT 59

US-10-229-915-22  
; Sequence 22, Application US/10229915  
; Publication No. US20030083262A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazarus, Douglas  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY  
; TITLE OF INVENTION: DISORDERS  
; FILE REFERENCE: PPI-127  
; CURRENT APPLICATION NUMBER: US/10/229,915  
; CURRENT FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: US 60/316,328  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 22  
;    LENGTH: 11  
;    TYPE: PRT  
;    ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: anti-inflammatory compound  
US-10-229-915-22

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 6 ARQ 8

RESULT 60

US-10-192-867-5

; Sequence 5, Application US/10192867  
; Publication No. US20030084466A1  
; GENERAL INFORMATION:  
; APPLICANT: BLUME-JENSEN, Peter  
; APPLICANT: HUNTER, Tony  
; TITLE OF INVENTION: SYSTEM AND METHOD FOR CONTROLLING MALE FERTILITY  
; FILE REFERENCE: SALKINS.002C1  
; CURRENT APPLICATION NUMBER: US/10/192,867  
; CURRENT FILING DATE: 2002-07-08  
; PRIOR APPLICATION NUMBER: US 60/175,625  
; 2000-01-11  
; PRIOR APPLICATION NUMBER: PCT/US01/00573  
; 2001-01-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Peptide  
; FEATURE:  
; NAME/KEY: PHOSPHORYLATION  
; LOCATION: 4  
; OTHER INFORMATION: Phosphorylated Tyrosine  
US-10-192-867-5

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 7 MKP 9

RESULT 61

US-10-211-088-297

; Sequence 297, Application US/10211088  
; Publication No. US20030104479A1  
; GENERAL INFORMATION:  
; APPLICANT: Bright, Gary R.



; APPLICANT: Premkumar, D. David  
 ; APPLICANT: Chen, Yih-Tai  
 ; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For  
 Molecular Binding  
 ; FILE REFERENCE: 01-1022-US  
 ; CURRENT APPLICATION NUMBER: US/10/211,088  
 ; CURRENT FILING DATE: 2002-10-15  
 ; PRIOR APPLICATION NUMBER: 60/309,395  
 ; PRIOR FILING DATE: 2001-08-01  
 ; PRIOR APPLICATION NUMBER: 60/341,589  
 ; PRIOR FILING DATE: 2001-12-13  
 ; NUMBER OF SEQ ID NOS: 366  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 297  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Protein-derived transport peptide  
 US-10-211-088-297

Query Match 27.3%; Score 3; DB 14; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
 |||  
 Db 6 ARQ 8

RESULT 62  
 US-10-136-738-3  
 ; Sequence 3, Application US/10136738  
 ; Publication No. US20030108886A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Finn, John  
 ; APPLICANT: MacLachlan, Ian  
 ; APPLICANT: Protiva Biotherapeutics Inc.  
 ; TITLE OF INVENTION: Autogene Nucleic Acids Encoding a  
 ; TITLE OF INVENTION: Secretable RNA Polymerase  
 ; FILE REFERENCE: 020801-000310US  
 ; CURRENT APPLICATION NUMBER: US/10/136,738  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/287,974  
 ; PRIOR FILING DATE: 2001-04-30  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: HIV-Tat variant secretion domain  
 US-10-136-738-3

Query Match 27.3%; Score 3; DB 14; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 6 ARQ 8

RESULT 63

US-10-072-602B-502

; Sequence 502, Application US/10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Utah Research Foundation  
; APPLICANT: Cognetix, Inc.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J, Michael  
; APPLICANT: Watkins, Maren  
; APPLICANT: Garrett, James E.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Grilley, Michelle  
; APPLICANT: Schoenfeld, Robert M.  
; APPLICANT: Walker, Craig  
; APPLICANT: Shetty, Reshma  
; APPLICANT: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US/10/072,602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 502  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Conus characteristicus  
US-10-072-602B-502

Query Match 27.3%; Score 3; DB 14; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PRR 10  
|||  
Db 3 PRR 5

RESULT 64

US-10-230-381-57

; Sequence 57, Application US/10230381  
; Publication No. US20030152591A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: New hepatitis C virus genotype 13, and its use as prophylactic,  
; TITLE OF INVENTION: therapeutic and diagnostic agents  
; FILE REFERENCE: INNX-124-EP

; CURRENT APPLICATION NUMBER: US/10/230,381  
; CURRENT FILING DATE: 2002-08-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
US-10-230-381-57

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 1 ARQ 3

RESULT 65

US-10-231-894-4

; Sequence 4, Application US/10231894  
; Publication No. US20030153490A1  
; GENERAL INFORMATION:  
; APPLICANT: Avrameas, Eustrate  
; TITLE OF INVENTION: Compositions and Methods of Treating Diabetes  
; FILE REFERENCE: 20440-004  
; CURRENT APPLICATION NUMBER: US/10/231,894  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 60/316,063  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus x Rattus norvegicus  
US-10-231-894-4

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQK 4  
|||  
Db 1 RQK 3

RESULT 66

US-10-286-457-327

; Sequence 327, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-P01-178

; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 327  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide  
libraries, based on  
; OTHER INFORMATION: ability to selectively bind to endothelial cells  
US-10-286-457-327

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 5 MKP 7

RESULT 67

US-10-286-457-646  
; Sequence 646, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND  
THERAPY  
; FILE REFERENCE: GPCI-P01-178  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 646  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide  
libraries, based on  
; OTHER INFORMATION: ability to selectively bind to endothelial cells  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(4)  
; OTHER INFORMATION: Xaa represents an amino acid with a small side chain,  
e.g., Ala o  
; OTHER INFORMATION: r Cys or Asp or Gly or Asn or Pro or Ser or Thr or Val  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (10)..(10)

; OTHER INFORMATION: Xaa represents any amino acid residue  
US-10-286-457-646

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MKP 8  
|||  
Db 5 MKP 7

RESULT 68

US-10-293-580-35

; Sequence 35, Application US/10293580  
; Publication No. US20030170767A1  
; GENERAL INFORMATION:  
; APPLICANT: Aurora Biosciences Corporation  
; APPLICANT: Cubitt, Andrew B.  
; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational  
Modifications  
; FILE REFERENCE: AURO1270 (08366/031001)  
; CURRENT APPLICATION NUMBER: US/10/293,580  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: US/09/129,192  
; PRIOR FILING DATE: 1998-07-24  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: phosphorylation site inserted at the N-terminus  
US-10-293-580-35

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RRS 11  
|||  
Db 4 RRS 6

RESULT 69

US-10-161-791-290

; Sequence 290, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.

```

; TITLE OF INVENTION:  SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION:  ISOLATING AND USING SAME
; NUMBER OF SEQUENCES:  467
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Pennie & Edmonds
;   STREET:  1155 Avenue of the Americas
;   CITY:  New York
;   STATE:  New York
;   COUNTRY:  U.S.A.
;   ZIP:  10036-2711
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/10/161,791
;   FILING DATE:
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/602,999
;   FILING DATE:  16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Misrock, S. Leslie
;   REGISTRATION NUMBER:  18,872
;   REFERENCE/DOCKET NUMBER:  1101-202
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 790-9090
;   TELEFAX:  (212) 869-9741/8864
;   TELEX:  66141 PENNIE
; INFORMATION FOR SEQ ID NO:  290:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  11 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  peptide
US-10-161-791-290

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Query Match          27.3%;  Score 3;  DB 14;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 7.8e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      8 PRR 10
      |||
Db      8 PRR 10

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RESULT 70
US-10-405-339-14
; Sequence 14, Application US/10405339
; Publication No. US20030190364A1
; GENERAL INFORMATION:
; APPLICANT: Panitch, Alyssa
; APPLICANT: Seal, Brandon
; TITLE OF INVENTION: Biological Affinity Based Delivery Systems
; FILE REFERENCE: 9138-0079US
; CURRENT APPLICATION NUMBER: US/10/405,339

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; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US 60/369,568  
; PRIOR FILING DATE: 2002-04-01  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
US-10-405-339-14

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARQ 3  
|||  
Db 6 ARQ 8

RESULT 71

US-10-231-889-4  
; Sequence 4, Application US/10231889  
; Publication No. US20030199677A1  
; GENERAL INFORMATION:  
; APPLICANT: Avrameas, Eustrate  
; APPLICANT: Ternynck, Therese  
; TITLE OF INVENTION: Amino Acid Sequences Facilitating Penetration Of A  
Substance Of Interest  
; TITLE OF INVENTION: Into Cells And/Or Nuclei  
; FILE REFERENCE: 20440-001  
; CURRENT APPLICATION NUMBER: US/10/231,889  
; CURRENT FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: PCT/FR00/02621  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: FR00/02621  
; PRIOR FILING DATE: 2000-03-01  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Mus musculus x Rattus norvegicus  
US-10-231-889-4

Query Match 27.3%; Score 3; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQK 4  
|||  
Db 1 RQK 3

RESULT 72

US-10-285-394-292

; Sequence 292, Application US/10285394  
; Publication No. US20030228583A1  
; GENERAL INFORMATION:  
; APPLICANT: AMACHER, DAVID E.  
; APPLICANT: FASULO, LISA M.  
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI  
; APPLICANT: HOLT, GORDON DUANE  
; APPLICANT: STIGER, THOMAS R.  
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE  
; FILE REFERENCE: POA-003.01  
; CURRENT APPLICATION NUMBER: US/10/285,394  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/335,964  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 412  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 292  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-285-394-292

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
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Db 9 KPR 11

RESULT 73

US-10-395-032-3080

; Sequence 3080, Application US/10395032  
; Publication No. US20030229199A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C9  
; CURRENT APPLICATION NUMBER: US/10/395,032  
; CURRENT FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3080  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-10-395-032-3080

Query Match 27.3%; Score 3; DB 15; Length 11;



Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 7 QKT 9

RESULT 74

US-10-395-032-3125  
; Sequence 3125, Application US/10395032  
; Publication No. US20030229199A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C9  
; CURRENT APPLICATION NUMBER: US/10/395,032  
; CURRENT FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3125  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-10-395-032-3125

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKT 5  
|||  
Db 7 QKT 9

RESULT 75

US-10-395-032-3170  
; Sequence 3170, Application US/10395032  
; Publication No. US20030229199A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C9  
; CURRENT APPLICATION NUMBER: US/10/395,032  
; CURRENT FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3170

; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Desmoglein cell adhesion recognition sequence  
US-10-395-032-3170

Query Match 27.3%; Score 3; DB 15; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QKT 5  
|||  
Db 7 QKT 9

Search completed: April 8, 2004, 16:35:45  
Job time : 31.3077 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds  
(without alignments)  
124.984 Million cell updates/sec

Title: US-09-787-443A-12  
Perfect score: 11  
Sequence: 1 ARQKTMKPRRS 11

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertibrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description
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1	3	27.3	11	2	Q47345	Q47345	escherichia
2	3	27.3	11	8	Q8SKP8	Q8skp8	ctenophorus
3	2	18.2	11	2	Q9R790	Q9r790	borrelia ga
4	2	18.2	11	2	Q8RKN1	Q8rkn1	escherichia
5	2	18.2	11	2	Q8L2T4	Q8l2t4	neisseria m
6	2	18.2	11	2	Q9R7U8	Q9r7u8	pseudomonas
7	2	18.2	11	2	Q9S618	Q9s618	prochloroco
8	2	18.2	11	2	P77404	P77404	escherichia
9	2	18.2	11	2	Q9RQ60	Q9rq60	buchnera ap
10	2	18.2	11	2	Q93RM6	Q93rm6	staphylococ
11	2	18.2	11	2	Q47600	Q47600	escherichia
12	2	18.2	11	2	Q9K332	Q9k332	staphylococ
13	2	18.2	11	2	Q44090	Q44090	acholeplasm
14	2	18.2	11	2	Q56413	Q56413	escherichia
15	2	18.2	11	2	Q9R872	Q9r872	escherichia
16	2	18.2	11	2	Q9R446	Q9r446	neisseria g
17	2	18.2	11	2	Q7X566	Q7x566	thermus the
18	2	18.2	11	3	Q9HFN8	Q9hfn8	candida rug
19	2	18.2	11	4	Q9Y3G2	Q9y3g2	homo sapien
20	2	18.2	11	4	Q9H4H5	Q9h4h5	homo sapien
21	2	18.2	11	4	Q15997	Q15997	homo sapien
22	2	18.2	11	4	Q9UCP5	Q9ucp5	homo sapien
23	2	18.2	11	5	Q26092	Q26092	pisaster oc
24	2	18.2	11	5	Q25916	Q25916	plasmodium
25	2	18.2	11	5	Q9NFX0	Q9nfx0	drosophila
26	2	18.2	11	5	Q8MPQ3	Q8mpq3	caenorhabdi
27	2	18.2	11	5	P82699	P82699	leucophaea
28	2	18.2	11	5	P82700	P82700	leucophaea
29	2	18.2	11	5	Q95PX6	Q95px6	caenorhabdi
30	2	18.2	11	6	Q9XSP7	Q9xsp7	pygathrix n
31	2	18.2	11	6	Q9XSP2	Q9xsp2	hylobates s
32	2	18.2	11	6	Q9XSP5	Q9xsp5	pan troglod
33	2	18.2	11	6	Q9XSP8	Q9xsp8	presbytis j
34	2	18.2	11	6	Q9XSP6	Q9xsp6	pongo pygma
35	2	18.2	11	6	Q9XSQ4	Q9xsq4	gorilla gor
36	2	18.2	11	7	O77872	O77872	oreochromis
37	2	18.2	11	7	O77873	O77873	oreochromis
38	2	18.2	11	7	O77871	O77871	oreochromis
39	2	18.2	11	8	Q94V94	Q94v94	varanus sto
40	2	18.2	11	8	Q9G5W2	Q9g5w2	laudakia tu
41	2	18.2	11	8	Q9G622	Q9g622	salea horsf
42	2	18.2	11	8	Q9G5Y6	Q9g5y6	agama agama
43	2	18.2	11	8	Q9G5W5	Q9g5w5	laudakia nu
44	2	18.2	11	8	Q8SKQ7	Q8skq7	ctenophorus
45	2	18.2	11	8	Q8WD08	Q8wd08	ctenophorus
46	2	18.2	11	8	O79985	O79985	laudakia ca
47	2	18.2	11	8	Q8SKQ4	Q8skq4	ctenophorus
48	2	18.2	11	8	Q9G359	Q9g359	japalura fl
49	2	18.2	11	8	Q8SKN6	Q8skn6	ctenophorus
50	2	18.2	11	8	Q9G649	Q9g649	otocryptis
51	2	18.2	11	8	Q9G5X4	Q9g5x4	trapelus ag
52	2	18.2	11	8	Q94V74	Q94v74	lanthanotus
53	2	18.2	11	8	Q8SKP2	Q8skp2	ctenophorus
54	2	18.2	11	8	Q8SKP5	Q8skp5	ctenophorus
55	2	18.2	11	8	Q9G350	Q9g350	laudakia sa
56	2	18.2	11	8	Q9G667	Q9g667	caimanops a
57	2	18.2	11	8	Q8WD17	Q8wd17	ctenophorus

58	2	18.2	11	8	Q9G670	Q9g670	rankinia ad
59	2	18.2	11	8	Q9G664	Q9g664	diporiphora
60	2	18.2	11	8	Q9G5Z8	Q9g5z8	acanthosaur
61	2	18.2	11	8	Q9G5W8	Q9g5w8	trapelus sa
62	2	18.2	11	8	Q9G371	Q9g371	pogona barb
63	2	18.2	11	8	Q9G353	Q9g353	trapelus sa
64	2	18.2	11	8	O79642	O79642	laudakia mi
65	2	18.2	11	8	Q8SKN9	Q8skn9	ctenophorus
66	2	18.2	11	8	Q94VH7	Q94vh7	varanus gil
67	2	18.2	11	8	Q9G619	Q9g619	ceratophora
68	2	18.2	11	8	Q9G2N4	Q9g2n4	chlamydosau
69	2	18.2	11	8	Q8WER7	Q8wer7	ceratophora
70	2	18.2	11	8	Q8WD50	Q8wd50	ceratophora
71	2	18.2	11	8	Q8SKQ1	Q8skq1	ctenophorus
72	2	18.2	11	8	O79639	O79639	laudakia le
73	2	18.2	11	8	Q9G676	Q9g676	amphiboluru
74	2	18.2	11	8	Q35374	Q35374	paramecium
75	2	18.2	11	8	Q9G5V0	Q9g5v0	laudakia st
76	2	18.2	11	8	Q9G5X1	Q9g5x1	trapelus pe
77	2	18.2	11	8	Q8WD29	Q8wd29	ctenophorus
78	2	18.2	11	8	Q8WD26	Q8wd26	ctenophorus
79	2	18.2	11	8	Q8WCZ9	Q8wcz9	ctenophorus
80	2	18.2	11	8	Q9G658	Q9g658	hydrosaurus
81	2	18.2	11	8	Q8WD14	Q8wd14	ctenophorus
82	2	18.2	11	8	Q8WER4	Q8wer4	ceratophora
83	2	18.2	11	8	Q9G673	Q9g673	ctenophorus
84	2	18.2	11	8	O79986	O79986	laudakia er
85	2	18.2	11	8	Q8WD02	Q8wd02	ctenophorus
86	2	18.2	11	8	Q8SKN3	Q8skn3	ctenophorus
87	2	18.2	11	8	Q8SKN0	Q8skn0	ctenophorus
88	2	18.2	11	8	Q9G655	Q9g655	japalura tr
89	2	18.2	11	8	Q9G637	Q9g637	calotes lio
90	2	18.2	11	8	Q8WD23	Q8wd23	ctenophorus
91	2	18.2	11	8	Q9G374	Q9g374	moloch horr
92	2	18.2	11	8	O79918	O79918	physignathu
93	2	18.2	11	8	Q9G5V9	Q9g5v9	laudakia st
94	2	18.2	11	8	Q9G688	Q9g688	physignathu
95	2	18.2	11	8	Q7Y9L3	Q7y9l3	amphiboluru
96	2	18.2	11	8	Q7Y9K9	Q7y9k9	amphiboluru
97	2	18.2	11	8	Q7Y9K0	Q7y9k0	diporiphora
98	2	18.2	11	8	Q7Y9J1	Q7y9j1	diporiphora
99	2	18.2	11	8	Q7Y9I8	Q7y9i8	diporiphora
100	2	18.2	11	8	Q7Y9I5	Q7y9i5	diporiphora

#### ALIGNMENTS

##### RESULT 1

Q47345

ID Q47345 PRELIMINARY; PRT; 11 AA.  
AC Q47345;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Leader peptide.  
OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RA Faber F., van Giezen M., Van Gorcom R.F.M., Harder W.;  
 RT "Identification of two Escherichia coli K12 proteins which are induced  
 RT in response to pollutant stress."  
 RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE OF 2-11 FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=85134883; PubMed=6396419;  
 RA Hudson G.S., Davidson B.E.;  
 RT "Nucleotide sequence and transcription of the phenylalanine and  
 RT tyrosine operons of Escherichia coli K12."  
 RL J. Mol. Biol. 180:1023-1051(1984).  
 DR EMBL; Z70523; CAA94435.1; -.  
 SQ SEQUENCE 11 AA; 1402 MW; 87AB199204141775 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRR 10  
 |||  
 Db 5 PRR 7

## RESULT 2

Q8SKP8

ID Q8SKP8 PRELIMINARY; PRT; 11 AA.  
 AC Q8SKP8;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Ctenophorus caudicinctus (Ring-tailed dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Ctenophorus.  
 OX NCBI\_TaxID=180905;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21623804; PubMed=11754013;  
 RA Melville J., Schulte J.A. II, Larson A.;  
 RT "A molecular phylogenetic study of ecological diversification in the  
 RT Australian lizard genus Ctenophorus."  
 RL J. Exp. Zool. 291:339-353(2001).  
 DR EMBL; AF375623; AAL78791.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1354 MW; A8F7371E33640336 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TMK 7  
|||  
Db 3 TMK 5

#### RESULT 3

Q9R790

ID Q9R790 PRELIMINARY; PRT; 11 AA.  
AC Q9R790;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Outer surface protein C (Fragment).  
GN OSPC.  
OS *Borrelia garinii*.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.  
OX NCBI\_TaxID=29519;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=G25;  
RX MEDLINE=97426044; PubMed=9282748;  
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,  
RA Rosa P.;  
RT "he *Borrelia burgdorferi* circular plasmid cp26: conservation of  
RT plasmid structure and targeted inactivation of the ospC gene.";  
RL Mol. Microbiol. 25:361-374(1997).  
DR EMBL; U93700; AAC45535.1; -.  
DR GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.  
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.  
DR GO; GO:0006952; P:defense response; IEA.  
DR InterPro; IPR001800; Lipoprotein\_6.  
DR Pfam; PF01441; Lipoprotein\_6; 1.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
||  
Db 1 MK 2

#### RESULT 4

Q8RKN1

ID Q8RKN1 PRELIMINARY; PRT; 11 AA.  
AC Q8RKN1;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Beta-lactamase CTX-M-9 (Fragment).

GN BLACTX-M-9.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=743-D;  
 RA Sabate M., Navarro F., Miro E., Campoy S., Mirelis B., Barbe J.,  
 RA Prats G.;  
 RT "A novel complex sull-type integron in Escherichia coli carrying the  
 RT bla(CTX-M-9) gene.";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY092058; AAM15718.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1071 MW; C26BF418D050440D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 4 AR 5

#### RESULT 5

Q8L2T4

ID Q8L2T4 PRELIMINARY; PRT; 11 AA.  
 AC Q8L2T4;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Histidinol phosphatase (Fragment).  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=126E;  
 RX MEDLINE=22051050; PubMed=12055303;  
 RA Zhu P., Klutch M.J., Bash M.C., Tsang R.S.W., Ng L.K., Tsai C.M.;  
 RT "Genetic Diversity of Three Lgt Loci for Biosynthesis of  
 RT Lipooligosaccharide (LOS) in Neisseria Species.";  
 RL Microbiology 148:1833-1844(2002).  
 DR EMBL; AF470685; AAM33538.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1273 MW; 01EC828D0AA72050 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
 ||  
 Db 1 MK 2



RESULT 6

Q9R7U8

ID Q9R7U8 PRELIMINARY; PRT; 11 AA.  
 AC Q9R7U8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE DNR protein (A regulatory protein for the expression of the Nir and  
 DE nor genes) (Fragment).  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PA01;  
 RX MEDLINE=95226457; PubMed=7711073;  
 RA Arai H., Igarashi Y., Kodama T.;  
 RT "The structural genes for nitric oxide reductase from Pseudomonas  
 RT aeruginosa.";  
 RL Biochim. Biophys. Acta 1261:279-284(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PA01;  
 RX MEDLINE=95394152; PubMed=7664887;  
 RA Arai H., Igarashi Y., Kodama T.;  
 RT "Expression of the nir and nor genes for denitrification of  
 RT Pseudomonas aeruginosa requires a novel CRP/FNR-related  
 RT transcriptional regulator, DNR, in addition to ANR.";  
 RL FEBS Lett. 371:73-76(1995).  
 DR EMBL; D50019; BAA08746.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 11 AA; 1543 MW; DF363CAE141B5736 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RR 10  
 ||  
 Db 7 RR 8

RESULT 7

Q9S618

ID Q9S618 PRELIMINARY; PRT; 11 AA.  
 AC Q9S618;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Cytochrome b6/f complex subunit IV (Fragment).  
 GN PETD.  
 OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.

OX NCBI\_TaxID=1220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in *Prochlorococcus* populations flow cytometrically  
 RT sorted from the Sargasso Sea and Gulf Stream.";  
 RL Limnol. Oceanog. 43:1615-1630(1998).  
 DR EMBL; AF070132; AAD20740.1; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
 ||  
 Db 6 KP 7

# RESULT 8

P77404

ID P77404 PRELIMINARY; PRT; 11 AA.  
 AC P77404;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE DNA sequence downstream of the ECOPRRI HSD locus (Fragment).  
 GN HSDR.  
 OS *Escherichia coli*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Escherichia*.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97206151; PubMed=9157244;  
 RA Tyndall C., Lehnherr H., Sandmeier U., Kulik E., Bickle T.A.;  
 RT "The type IC hsd loci of the enterobacteria are flanked by DNA with  
 RT high homology to the phage P1 genome: implications for the evolution  
 RT and spread of DNA restriction systems.";  
 RL Mol. Microbiol. 23:729-736(1997).  
 DR EMBL; X98145; CAA66840.1; -.  
 DR EMBL; X98144; CAA66839.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1259 MW; 714AB092A4072734 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
 ||  
 Db 7 RS 8

# RESULT 9

Q9RQ60

ID Q9RQ60 PRELIMINARY; PRT; 11 AA.  
AC Q9RQ60;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE Acetohydroxy acid synthase small subunit (Fragment).  
GN ILVH.  
OS Buchnera aphidicola.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Buchnera.  
OX NCBI\_TaxID=9;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20022990; PubMed=10555290;  
RA Clark M.A., Moran N.A., Baumann P.;  
RT "Sequence evolution in bacterial endosymbionts having extreme base  
compositions.";  
RL Mol. Biol. Evol. 16:1586-1598(1999).  
DR EMBL; AF129503; AAF13796.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1330 MW; 0E89EF1E2045B050 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
||  
Db 1 MK 2

# RESULT 10

Q93RM6

ID Q93RM6 PRELIMINARY; PRT; 11 AA.  
AC Q93RM6;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Lipophilic protein affecting bacterial lysis and methicillin  
resistance (Fragment).  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SRM551;  
RA Maki H.;  
RT "Upstream region of 11m gene.";  
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AB000542; BAB62080.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1191 MW; 4AC763F4C2C72727 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 10 TM 11

RESULT 11

Q47600

ID Q47600 PRELIMINARY; PRT; 11 AA.  
AC Q47600;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE REase protein (Fragment).  
GN REASE.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao T., Bourne J.C., Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-  
RT modification systems.";  
RL J. Bacteriol. 173:1367-1375(1991).  
DR EMBL; M63619; AAA24556.1; -.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1232 MW; 63175479572AB5A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
||  
Db 4 RS 5

RESULT 12

Q9K332

ID Q9K332 PRELIMINARY; PRT; 11 AA.  
AC Q9K332;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Geh (Fragment).  
GN GEH.  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VARIOUS STRAINS;  
RX MEDLINE=20187516; PubMed=10722640;  
RA Cramton S.E., Schnell N.F., Gotz F., Bruckner R.;  
RT "Identification of a new repetitive element in Staphylococcus  
RT aureus.";

RL Infect. Immun. 68:2344-2348(2000).  
DR EMBL; AF195967; AAF60251.1; -.  
DR EMBL; AF195963; AAF60243.1; -.  
DR EMBL; AF195964; AAF60245.1; -.  
DR EMBL; AF195965; AAF60247.1; -.  
DR EMBL; AF195966; AAF60249.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1262 MW; 4F978F86AAB1A723 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KT 5  
||  
Db 1 KT 2

RESULT 13

Q44090

ID Q44090 PRELIMINARY; PRT; 11 AA.  
AC Q44090;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical export segment (Fragment).  
OS Acholeplasma laidlawii.  
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;  
OC Acholeplasmataceae; Acholeplasma.  
OX NCBI\_TaxID=2148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A-EF22;  
RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;  
RT "Sequence regions from Acholeplasma laidlawii which restore export of  
RT beta-lactamase in Escherichia coli.";  
RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; Z22875; CAA80495.1; -.  
DR PIR; S33519; S33519.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
||  
Db 1 MK 2

RESULT 14

Q56413

ID Q56413 PRELIMINARY; PRT; 11 AA.  
AC Q56413;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE IS602L region DNA, 5' end (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Transposon Tn602;  
 RX MEDLINE=87318208; PubMed=2819910;  
 RA Stibitz S., Davies J.E.;  
 RT "Tn602: A naturally occurring relative of Tn903 with direct repeats."  
 RL Plasmid 17:202-209(1987).  
 DR EMBL; M22735; AAA27464.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1361 MW; 447E8354A05339C3 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QK 4  
 ||  
 Db 3 QK 4

# RESULT 15

Q9R872

ID Q9R872 PRELIMINARY; PRT; 11 AA.  
 AC Q9R872;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Dihydrofolate reductase (Fragment).  
 GN DFR1.  
 OS Escherichia coli.  
 OG Plasmid r483.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Tn7;  
 RA Hansson K., Sundstrom L., Pelletier A., Roy P.H.;  
 RT "Sequence and function of the second type of integron in Tn7."  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Tn7;  
 RX MEDLINE=82220022; PubMed=6283361;  
 RA Lichtenstein C., Brenner S.;  
 RT "Unique insertion site of Tn7 in the E. coli chromosome."  
 RL Nature 297:601-603(1982).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Tn7;

RX MEDLINE=83290694; PubMed=6411680;  
 RA Simonsen C.C., Chen E.Y., Levinson A.D.;  
 RT "Identification of the type I trimethoprim-resistant dihydrofolate  
 RT reductase specified by the Escherichia coli R-plasmid R483: Comparison  
 RT with procaryotic and eucaryotic dihydrofolate reductases.";  
 RL J. Bacteriol. 155:1001-1008(1983).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON=Tn7;  
 RX MEDLINE=83272957; PubMed=6308574;  
 RA Fling M.E., Richards C.;  
 RT "The nucleotide sequence of the trimethoprim-resistant dihydrofolate  
 RT reductase gene harbored by Tn7.";  
 RL Nucleic Acids Res. 11:5147-5158(1983).  
 DR EMBL; AJ001816; CAA05032.1; -.  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KW Plasmid.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1221 MW; 92014864C2C69735 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
 ||  
 Db 1 MK 2

# RESULT 16

Q9R446

ID Q9R446 PRELIMINARY; PRT; 11 AA.  
 AC Q9R446;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Carbamoyl-phosphate synthase subunit A (Fragment).  
 GN CARA.  
 OS Neisseria gonorrhoeae.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=485;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MS11, and FA1090;  
 RX MEDLINE=95291461; PubMed=7773412;  
 RA Lawson F.S., Billowes F.M., Dillon J.A.;  
 RT "Organization of carbamoyl-phosphate synthase genes in Neisseria  
 RT gonorrhoeae includes a large, variable intergenic sequence which is  
 RT also present in other Neisseria species.";  
 RL Microbiology 141:0-0(0).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MS11, and FA1090;  
 RA Brinkman F.S.L., Francis F.M., Dillon J.R.;  
 RT "Complexity of the variable sequence between the carbamoyl-phosphate  
 RT synthase genes of Neisseria species.";

RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF029363; AAC78453.1; -.  
DR EMBL; AF029362; AAC78452.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DDD33694 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
||  
Db 5 MK 6

RESULT 17

Q7X566

ID Q7X566 PRELIMINARY; PRT; 11 AA.  
AC Q7X566;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein (Fragment).  
OS Thermus thermophilus.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
OC Thermus.  
OX NCBI\_TaxID=274;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Miyazaki T., Miyazaki J., Nishiyama M., Yamane H.;  
RT "Characterization of a LysN, the 4th enzyme in lysine biosynthesis, in  
RT an extremely thermophilic bacterium, Thermus thermophilus HB27.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AB097117; BAC76940.1; -.  
KW Hypothetical protein.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1073 MW; 39792C1E75B72EB8 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
||  
Db 9 KP 10

RESULT 18

Q9HFN8

ID Q9HFN8 PRELIMINARY; PRT; 11 AA.  
AC Q9HFN8;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Acyl carrier protein (Fragment).  
GN ACP.  
OS Candida rugosa (Yeast) (Candida cylindracea).



OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=5481;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Biasio W.;  
 RL Thesis (2000), University of Vienna, Austria.  
 DR EMBL; AJ279021; CAC08812.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1274 MW; D2E4CC3976C40732 CRC64;

Query Match 18.2%; Score 2; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQ 3  
 ||  
 Db 6 RQ 7

# RESULT 19

Q9Y3G2

ID Q9Y3G2 PRELIMINARY; PRT; 11 AA.  
 AC Q9Y3G2;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE LSFR2 protein (Fragment).  
 GN LSFR2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99299247; PubMed=10369878;  
 RA Gilley J., Fried M.;  
 RT "Extensive gene order differences within regions of conserved synteny  
 RT between the Fugu and human genomes: implications for chromosomal  
 RT evolution and the cloning of disease genes."  
 RL Hum. Mol. Genet. 8:1313-1320(1999).  
 DR EMBL; Y17456; CAB44349.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1342 MW; 68C5E5D7A8772324 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RQ 3  
 ||  
 Db 2 RQ 3

# RESULT 20

Q9H4H5

ID Q9H4H5 PRELIMINARY; PRT; 11 AA.  
 AC Q9H4H5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE DJ661I20.2 (Novel helicase C-terminal domain and SNF2 N-terminal  
 DE domains containing protein) (Fragment).  
 GN DJ620E11.1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Skuce C.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AL031669; CAC17164.2; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1420 MW; 5EB2C32A3326D053 CRC64;  
  
 Query Match 18.2%; Score 2; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 6 MK 7  
 ||  
 Db 1 MK 2

RESULT 21

Q15997  
 ID Q15997 PRELIMINARY; PRT; 11 AA.  
 AC Q15997;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE RARA protein (Fragment).  
 GN RARA.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93222087; PubMed=7682097;  
 RA Dong S., Geng J.P., Tong J.H., Wu Y., Cai J.R., Sun G.L., Chen S.R.,  
 RA Wang Z.Y., Larsen C.J., Berger R., et al;  
 RT "Breakpoint clusters of the PML gene in acute promyelocytic leukemia:  
 RT primary structure of the reciprocal products of the PML-RARA gene in a  
 RT patient with t(15;17)."  
 RL Genes Chromosomes Cancer 6:133-139(1993).  
 DR EMBL; S57794; AAD13888.1; -.  
 DR PIR; I54081; I54081.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 11 AA; 1277 MW; 33C70E22CDDDC417 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 4 PR 5

RESULT 22

Q9UCP5

ID Q9UCP5 PRELIMINARY; PRT; 11 AA.  
AC Q9UCP5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE AggreCAN core protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92235266; PubMed=1569188;  
RA Sandy J.D., Flannery C.R., Neame P.J., Lohmander L.S.;  
RL J. Clin. Invest. 89:1512-1516(1992).  
DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.  
DR GO; GO:0001501; P:skeletal development; NAS.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1149 MW; 8FBFE8DFE72042D5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 1 AR 2

RESULT 23

Q26092

ID Q26092 PRELIMINARY; PRT; 11 AA.  
AC Q26092;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Sea StAR histone H2B gene 5'region (Fragment).  
OS Pisaster ochraceus (Sea star).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;  
OC Asteroidea; Forcipulatacea; Forcipulatida; Asteroidea; Pisaster.  
OX NCBI\_TaxID=7612;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Sperm;

RA Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;  
 RT "Organization and Unusual Expression of Histone Genes in the Sea Star  
 RT *Pisaster ochraceus*.";  
 RL J. Mol. Evol. 25:29-36(1987).  
 DR EMBL; X05619; CAA29106.1; -.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QK 4  
 ||  
 Db 10 QK 11

#### RESULT 24

Q25916

ID Q25916 PRELIMINARY; PRT; 11 AA.  
 AC Q25916;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Malaria antigen (7H8/2) (Fragment).  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91164876; PubMed=1706114;  
 RA Limpiaiboon T., Taylor D., Jones G., Geysen H.M., Saul A.;  
 RT "Characterization of a Plasmodium falciparum epitope recognized by a  
 RT monoclonal antibody with broad isolate and species specificity.";  
 RL Southeast Asian J. Trop. Med. Public Health 21:388-396(1990).  
 DR EMBL; M31305; AAA29645.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 11 AA; 1415 MW; DB03D3BC42C33699 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MK 7  
 ||  
 Db 5 MK 6

#### RESULT 25

Q9NFX0

ID Q9NFX0 PRELIMINARY; PRT; 11 AA.  
 AC Q9NFX0;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Mitochondrial aconitase (Fragment).  
 GN ACON OR MAC OR CG9244.

OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; *Drosophila*.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CANTON S;  
 RA Lind M.I.;  
 RT "Characterisation of two iron regulatory proteins and mitochondrial  
 RT aconitase in *Drosophila melanogaster*.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AJ252019; CAB93522.1; -.  
 DR FlyBase; FBgn0010100; Acon.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1204 MW; 7C889CE4D4469734 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 3 AR 4

# RESULT 26

## Q8MPQ3

ID Q8MPQ3 PRELIMINARY; PRT; 11 AA.  
 AC Q8MPQ3;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein Y23H5A.8b.  
 GN Y23H5A.8.  
 OS *Caenorhabditis elegans*.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA Waterston R.;  
 RT "Genome sequence of the nematode *C. elegans*: a platform for  
 RT investigating biology. The *C. elegans* Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Dempsey S., Le T.T.;  
 RT "The sequence of *C. elegans* cosmid Y23H5A.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF077541; AAM54173.1; -.  
DR WormPep; Y23H5A.8b; CE31097.  
KW Hypothetical protein.  
SQ SEQUENCE 11 AA; 1319 MW; 6920D63A21B77414 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RR 10  
||  
Db 4 RR 5

RESULT 27

P82699

ID P82699 PRELIMINARY; PRT; 11 AA.  
AC P82699;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Periviscerokinin-2 (LEM-PVK-2).  
OS Leucophaea maderae (Madeira cockroach),  
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),  
OS Blaberus craniifer,  
OS Blaptica dubia, and  
OS Gromphadorina portentosa (Cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988, 6990, 6982, 132935, 36953;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.  
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;  
RX MEDLINE=20307624; PubMed=10849006;  
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;  
RT "Identification of novel periviscerokinins from single neurohaemal  
RT release sites in insects. MS/MS fragmentation complemented by Edman  
RT degradation.";  
RL Eur. J. Biochem. 267:3869-3873(2000).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -!- MASS SPECTROMETRY: MW=1102.6; METHOD=MALDI.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1103 MW; 2F4D9FFD85B05728 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 9 PR 10

## RESULT 28

P82700

ID P82700 PRELIMINARY; PRT; 11 AA.  
 AC P82700;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Periviscerokinin-3 (LEM-PVK-3).  
 OS Leucophaea maderae (Madeira cockroach),  
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),  
 OS Blaberus craniifer,  
 OS Blaptica dubia (Argentinian wood cockroach), and  
 OS Gromphadorina portentosa (Cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988, 6990, 6982, 132935, 36953;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.  
 RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;  
 RX MEDLINE=20307624; PubMed=10849006;  
 RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;  
 RT "Identification of novel periviscerokinins from single neurohaemal  
 RT release sites in insects. MS/MS fragmentation complemented by Edman  
 RT degradation.";  
 RL Eur. J. Biochem. 267:3869-3873(2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
 ||  
 Db 9 PR 10

## RESULT 29

Q95PX6

ID Q95PX6 PRELIMINARY; PRT; 11 AA.  
 AC Q95PX6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN ZK1236.8.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode *C. elegans*: a platform for  
 RT investigating biology. The *C. elegans* Sequencing Consortium."  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Favello A.;  
 RT "The sequence of *C. elegans* cosmid ZK1236."  
 RL Submitted (MAY-1993) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Bristol N2;  
 RA Waterston R.;  
 RT "Direct Submission."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; L13200; AAL11108.1; -.  
 DR WormPep; ZK1236.8; CE29629.  
 KW Hypothetical protein.  
 SQ SEQUENCE 11 AA; 1304 MW; DFA3510A25A76322 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
 ||  
 Db 5 KP 6

# RESULT 30

## Q9XSP7

ID Q9XSP7 PRELIMINARY; PRT; 11 AA.  
 AC Q9XSP7;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Platelet-derived growth factor A chain (Fragment).  
 GN PDGFA.  
 OS *Pygathrix nemaeus* (Dove langur).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;  
 OC *Pygathrix*.  
 OX NCBI\_TaxID=54133;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065871; PubMed=10598812;  
 RA Bonthron D.T., Smith S.L., Campbell R.;  
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
 RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243282; CAB45924.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11



SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
||  
Db 8 RS 9

RESULT 31

Q9XSP2

ID Q9XSP2 PRELIMINARY; PRT; 11 AA.  
AC Q9XSP2;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Platelet-derived growth factor A chain (Fragment).  
GN PDGFA.  
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
OX NCBI\_TaxID=9590;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20065871; PubMed=10598812;  
RA Bonthron D.T., Smith S.L., Campbell R.;  
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";  
RL Hum. Genet. 105:452-459(1999).  
DR EMBL; AJ243280; CAB45927.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
||  
Db 8 RS 9

RESULT 32

Q9XSP5

ID Q9XSP5 PRELIMINARY; PRT; 11 AA.  
AC Q9XSP5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Platelet-derived growth factor A chain (Fragment).  
GN PDGFA.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065871; PubMed=10598812;  
 RA Bonthron D.T., Smith S.L., Campbell R.;  
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
 RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243277; CAB45926.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
 ||  
 Db 8 RS 9

# RESULT 33

## Q9XSP8

ID Q9XSP8 PRELIMINARY; PRT; 11 AA.  
 AC Q9XSP8;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Platelet-derived growth factor A chain (Fragment).  
 GN PDGFA.  
 OS Presbytis johnii.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;  
 OC Presbytis.  
 OX NCBI\_TaxID=98375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065871; PubMed=10598812;  
 RA Bonthron D.T., Smith S.L., Campbell R.;  
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
 RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243281; CAB46013.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
 ||  
 Db 8 RS 9

# RESULT 34

## Q9XSP6

ID Q9XSP6 PRELIMINARY; PRT; 11 AA.

AC Q9XSP6;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Platelet-derived growth factor A chain (Fragment).  
 GN PDGFA.  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 OX NCBI\_TaxID=9600;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065871; PubMed=10598812;  
 RA Bonthron D.T., Smith S.L., Campbell R.;  
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
 RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243279; CAB45925.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
 ||  
 Db 8 RS 9

# RESULT 35

Q9XSQ4  
 ID Q9XSQ4 PRELIMINARY; PRT; 11 AA.  
 AC Q9XSQ4;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Platelet-derived growth factor A chain (Fragment).  
 GN PDGFA.  
 OS Gorilla gorilla (gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 OX NCBI\_TaxID=9593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20065871; PubMed=10598812;  
 RA Bonthron D.T., Smith S.L., Campbell R.;  
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."  
 RL Hum. Genet. 105:452-459(1999).  
 DR EMBL; AJ243278; CAB45916.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
||  
Db 8 RS 9

RESULT 36

O77872

ID O77872 PRELIMINARY; PRT; 11 AA.  
AC O77872;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 1 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci.";  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF049981; AAC41320.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
||  
Db 8 KP 9

RESULT 37

O77873

ID O77873 PRELIMINARY; PRT; 11 AA.  
AC O77873;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 1 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci.";  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF049982; AAC41321.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
 ||  
 Db 8 KP 9

# RESULT 38

O77871

ID O77871 PRELIMINARY; PRT; 11 AA.  
 AC O77871;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 1 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
 RT class II B loci.";  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF049980; AAC41319.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1133 MW; 283248EC3EB72728 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
 ||  
 Db 8 KP 9

RESULT 39

Q94V94

ID Q94V94 PRELIMINARY; PRT; 11 AA.  
 AC Q94V94;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Varanus storri.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.  
 OX NCBI\_TaxID=169855;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ast J.C.;  
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
 RL Cladistics 17:0-0(2001).  
 DR EMBL; AF407531; AAL10145.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1387 MW; 8CBDEE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 10 TM 11

RESULT 40

Q9G5W2

ID Q9G5W2 PRELIMINARY; PRT; 11 AA.  
 AC Q9G5W2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Laudakia tuberculata.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC Laudakia.  
 OX NCBI\_TaxID=118215;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128514; AAG00779.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1327 MW; A8F7371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

# RESULT 41

Q9G622

ID Q9G622 PRELIMINARY; PRT; 11 AA.  
 AC Q9G622;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Salea horsfieldii.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
 OC Salea.  
 OX NCBI\_TaxID=118233;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128490; AAG00707.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 5 AR 6

RESULT 42

Q9G5Y6

ID Q9G5Y6 PRELIMINARY; PRT; 11 AA.  
AC Q9G5Y6;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Agama agama (Red-headed rock agama).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Agama.  
OX NCBI\_TaxID=103336;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and information content of the mitochondrial genomic  
RT structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
RT phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128504; AAG00749.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1324 MW; 9D52EC1E336415A1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KT 5  
||  
Db 3 KT 4

RESULT 43

Q9G5W5

ID Q9G5W5 PRELIMINARY; PRT; 11 AA.



AC Q9G5W5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Laudakia nupta.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC Laudakia.  
 OX NCBI\_TaxID=118212;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128513; AAG00776.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

#### RESULT 44

Q8SKQ7

ID Q8SKQ7 PRELIMINARY; PRT; 11 AA.  
 AC Q8SKQ7;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Ctenophorus clayi (Black-shouldered ground dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Ctenophorus.  
 OX NCBI\_TaxID=180906;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21623804; PubMed=11754013;  
 RA Melville J., Schulte J.A. II, Larson A.;  
 RT "A molecular phylogenetic study of ecological diversification in the  
 RT Australian lizard genus Ctenophorus."  
 RL J. Exp. Zool. 291:339-353(2001).  
 DR EMBL; AF375620; AAL78782.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1340 MW; A8F7371E33640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

# RESULT 45

Q8WD08

ID Q8WD08 PRELIMINARY; PRT; 11 AA.  
 AC Q8WD08;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Ctenophorus tjantjalka.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Ctenophorus.  
 OX NCBI\_TaxID=180007;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Melville J., Schulte J.A. II, Larson A.;  
 RT "A molecular phylogenetic study of ecological diversification in the  
 RT Australian lizard genus Ctenophorus."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF375637; AAL40442.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1340 MW; A8F7371E33640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

RESULT 46

079985

ID 079985 PRELIMINARY; PRT; 11 AA.  
 AC 079985;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome C oxidase subunit I (Fragment).  
 GN COI.  
 OS Laudakia caucasia.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC Laudakia.  
 OX NCBI\_TaxID=71145;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98424476; PubMed=9751922;  
 RA Macey J.R., Schulte J.A. II, Ananjeva N.B., Larson A.,  
 RA Rastegar-Pouyani N., Shammakov S.M., Papenfuss T.J.;  
 RT "Phylogenetic relationships among Agamid lizards of the Laudakia  
 RT caucasia species group: testing hypotheses of biogeographic  
 RT fragmentation and an area cladogram for the Iranian Plateau.";  
 RL Mol. Phylogenet. Evol. 10:118-131(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20179532; PubMed=10712852;  
 RA Macey J.R., Schulte J.A. II, Kami H.G., Ananjeva N.B., Larson A.,  
 RA Papenfuss T.J.;  
 RT "Testing hypotheses of vicariance in the agamid lizard laudakia  
 RT caucasia from mountain ranges on the northern iraninan plateau.";  
 RL Mol. Phylogenet. Evol. 14:479-483(2000).  
 DR EMBL; AF028687; AAC99614.1; -.  
 DR EMBL; AF028681; AAC99596.1; -.  
 DR EMBL; AF028682; AAC99599.1; -.  
 DR EMBL; AF028683; AAC99602.1; -.  
 DR EMBL; AF028684; AAC99605.1; -.  
 DR EMBL; AF028685; AAC99608.1; -.  
 DR EMBL; AF028686; AAC99611.1; -.  
 DR EMBL; AF172705; AAF65208.1; -.  
 DR EMBL; AF172704; AAF65205.1; -.  
 DR PIR; T12264; T12264.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

RESULT 47

Q8SKQ4

ID Q8SKQ4 PRELIMINARY; PRT; 11 AA.  
 AC Q8SKQ4;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Ctenophorus maculosus (Lake Eyre dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Ctenophorus.  
 OX NCBI\_TaxID=180913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21623804; PubMed=11754013;  
 RA Melville J., Schulte J.A. II, Larson A.;  
 RT "A molecular phylogenetic study of ecological diversification in the  
 RT Australian lizard genus Ctenophorus."  
 RL J. Exp. Zool. 291:339-353(2001).  
 DR EMBL; AF375621; AAL78785.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1340 MW; A8F7371E33640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

RESULT 48

Q9G359

ID Q9G359 PRELIMINARY; PRT; 11 AA.  
 AC Q9G359;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Japalura flaviceps.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
 OC Japalura.  
 OX NCBI\_TaxID=52218;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97153820; PubMed=9000751;  
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
 RT "Replication slippage may cause parallel evolution in the secondary

RT structures of mitochondrial transfer RNAs.";  
 RL Mol. Biol. Evol. 14:30-39(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128500; AAG00737.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1341 MW; 538E371E33640DD7 CRC64;  
  
 Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 AR 2  
 ||  
 Db 5 AR 6

# RESULT 49

Q8SKN6

ID Q8SKN6 PRELIMINARY; PRT; 11 AA.  
 AC Q8SKN6;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Ctenophorus femoralis (Long-tailed sand dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Ctenophorus.  
 OX NCBI\_TaxID=180908;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21623804; PubMed=11754013;  
 RA Melville J., Schulte J.A. II, Larson A.;  
 RT "A molecular phylogenetic study of ecological diversification in the  
 RT Australian lizard genus Ctenophorus.";  
 RL J. Exp. Zool. 291:339-353(2001).  
 DR EMBL; AF375627; AAL78803.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.

FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1374 MW; A8F73710D3640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

#### RESULT 50

Q9G649

ID Q9G649 PRELIMINARY; PRT; 11 AA.  
AC Q9G649;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Otocryptis wiegmanni.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Otocryptis.  
OX NCBI\_TaxID=118220;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and information content of the mitochondrial genomic  
RT structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
RT phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128480; AAG00677.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1347 MW; 932D3710D3640DC1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 5 AR 6

RESULT 51

Q9G5X4

ID Q9G5X4 PRELIMINARY; PRT; 11 AA.  
 AC Q9G5X4;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Trapelus agilis.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC Trapelus.  
 OX NCBI\_TaxID=52210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128509; AAG00764.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1391 MW; BFC73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

RESULT 52

Q94V74

ID Q94V74 PRELIMINARY; PRT; 11 AA.  
 AC Q94V74;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Lanthanotus borneensis.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Lanthanotidae;  
 OC Lanthanotus.  
 OX NCBI\_TaxID=62058;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ast J.C.;  
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
 RL Cladistics 17:0-0(2001).  
 DR EMBL; AF407541; AAL10175.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1388 MW; 8F28EE80C7336411 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 2 TM 3

# RESULT 53

Q8SKP2

ID Q8SKP2 PRELIMINARY; PRT; 11 AA.  
 AC Q8SKP2;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Ctenophorus gibba (Bulldust ground dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Ctenophorus.  
 OX NCBI\_TaxID=180910;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21623804; PubMed=11754013;  
 RA Melville J., Schulte J.A. II, Larson A.;  
 RT "A molecular phylogenetic study of ecological diversification in the  
 RT Australian lizard genus Ctenophorus.";  
 RL J. Exp. Zool. 291:339-353(2001).  
 DR EMBL; AF375625; AAL78797.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1374 MW; A8F73710D3640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||



Db

3 TM 4

RESULT 54

Q8SKP5

ID Q8SKP5 PRELIMINARY; PRT; 11 AA.  
AC Q8SKP5;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Ctenophorus ornatus (Ornate dragon).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
OC Ctenophorus.  
OX NCBI\_TaxID=95347;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21623804; PubMed=11754013;  
RA Melville J., Schulte J.A. II, Larson A.;  
RT "A molecular phylogenetic study of ecological diversification in the  
RT Australian lizard genus Ctenophorus."  
RL J. Exp. Zool. 291:339-353(2001).  
DR EMBL; AF375624; AAL78794.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1340 MW; A8F7371E33640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TM 6  
||  
Db 3 TM 4

RESULT 55

Q9G350

ID Q9G350 PRELIMINARY; PRT; 11 AA.  
AC Q9G350;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Laudakia sacra.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
OC Laudakia.  
OX NCBI\_TaxID=52204;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=97153820; PubMed=9000751;  
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
 RT "Replication slippage may cause parallel evolution in the secondary  
 RT structures of mitochondrial transfer RNAs.";  
 RL Mol. Biol. Evol. 14:30-39(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128515; AAG00782.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

# RESULT 56

Q9G667

ID Q9G667 PRELIMINARY; PRT; 11 AA.  
 AC Q9G667;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Caimanops amphiboluroides (Mulga dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Caimanops.  
 OX NCBI\_TaxID=118092;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128472; AAG00653.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1340 MW; A8F7371E33640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

# RESULT 57

Q8WD17  
 ID Q8WD17 PRELIMINARY; PRT; 11 AA.  
 AC Q8WD17;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Ctenophorus reticulatus (Western netted dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Ctenophorus.  
 OX NCBI\_TaxID=180002;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Melville J., Schulte J.A. II, Larson A.;  
 RT "A molecular phylogenetic study of ecological diversification in the  
 RT Australian lizard genus Ctenophorus.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF375634; AAL40433.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1313 MW; A8F7371E336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

RESULT 58

Q9G670

ID Q9G670 PRELIMINARY; PRT; 11 AA.  
 AC Q9G670;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Rankinia adelaidensis (Heath dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Rankinia.  
 OX NCBI\_TaxID=118249;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128471; AAG00650.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1340 MW; A8F7371E33640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

RESULT 59

Q9G664

ID Q9G664 PRELIMINARY; PRT; 11 AA.  
 AC Q9G664;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Diporiphora bilineata (Two-lined dragon).

OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Diporiphora.  
 OX NCBI\_TaxID=118204;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128473; AAG00656.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1340 MW; A8F7371E33640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

# RESULT 60

Q9G5Z8

ID Q9G5Z8 PRELIMINARY; PRT; 11 AA.  
 AC Q9G5Z8;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Acanthosaura lepidogaster.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
 OC Acanthosaura.  
 OX NCBI\_TaxID=118088;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128499; AAG00734.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1279 MW; 5DF7371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2  
 ||  
 Db 5 AR 6

# RESULT 61

Q9G5W8  
 ID Q9G5W8 PRELIMINARY; PRT; 11 AA.  
 AC Q9G5W8;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Trapelus savignyi.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC Trapelus.  
 OX NCBI\_TaxID=118240;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128512; AAG00773.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

RESULT 62

Q9G371

ID Q9G371 PRELIMINARY; PRT; 11 AA.  
AC Q9G371;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Pogona barbata (Bearded dragon).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
OC Pogona.  
OX NCBI\_TaxID=52202;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97153820; PubMed=9000751;  
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
RT "Replication slippage may cause parallel evolution in the secondary  
RT structures of mitochondrial transfer RNAs.";  
RL Mol. Biol. Evol. 14:30-39(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and information content of the mitochondrial genomic  
RT structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
RT phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128474; AAG00659.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1340 MW; A8F7371E33640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

RESULT 63

Q9G353

ID Q9G353 PRELIMINARY; PRT; 11 AA.  
AC Q9G353;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Trapelus sanguinolentus.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
OC Trapelus.  
OX NCBI\_TaxID=118238;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97153820; PubMed=9000751;  
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
RT "Replication slippage may cause parallel evolution in the secondary  
RT structures of mitochondrial transfer RNAs.";  
RL Mol. Biol. Evol. 14:30-39(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and information content of the mitochondrial genomic  
RT structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
RT phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128511; AAG00770.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1361 MW; A8F73710D36411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4



## RESULT 64

O79642

ID O79642 PRELIMINARY; PRT; 11 AA.  
 AC O79642;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS *Laudakia microlepis*.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
 OC *Laudakia*.  
 OX NCBI\_TaxID=71149;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98424476; PubMed=9751922;  
 RA Macey J.R., Schulte J.A. II, Ananjeva N.B., Larson A.,  
 RA Rastegar-Pouyani N., Shammakov S.M., Papenfuss T.J.;  
 RT "Phylogenetic relationships among Agamid lizards of the *Laudakia*  
 RT *caucasia* species group: testing hypotheses of biogeographic  
 RT fragmentation and an area cladogram for the Iranian Plateau."  
 RL Mol. Phylogenet. Evol. 10:118-131(1998).  
 DR EMBL; AF028678; AAC99587.1; -.  
 DR PIR; T12248; T12248.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1327 MW; A8F7371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TM 6  
 ||  
 Db 3 TM 4

## RESULT 65

Q8SKN9

ID Q8SKN9 PRELIMINARY; PRT; 11 AA.  
 AC Q8SKN9;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS *Ctenophorus fordi* (Mallee dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC *Ctenophorus*.  
 OX NCBI\_TaxID=180909;  
 RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=21623804; PubMed=11754013;  
RA Melville J., Schulte J.A. II, Larson A.;  
RT "A molecular phylogenetic study of ecological diversification in the  
RT Australian lizard genus Ctenophorus.";  
RL J. Exp. Zool. 291:339-353(2001).  
DR EMBL; AF375626; AAL78800.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1374 MW; A8F73710D3640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

# RESULT 66

Q94VH7

ID Q94VH7 PRELIMINARY; PRT; 11 AA.  
AC Q94VH7;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Varanus gilleni (Pygmy mulga monitor).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.  
OX NCBI\_TaxID=169840;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ast J.C.;  
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
RL Cladistics 17:0-0(2001).  
DR EMBL; AF407499; AAL10051.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1340 MW; CF6DEE80C733640D CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 4 AR 5

# RESULT 67

Q9G619

ID Q9G619 PRELIMINARY; PRT; 11 AA.  
AC Q9G619;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Ceratophora aspera.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Ceratophora.  
OX NCBI\_TaxID=118195;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and information content of the mitochondrial genomic  
RT structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
RT phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128491; AAG00710.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 5 AR 6

#### RESULT 68

Q9G2N4  
ID Q9G2N4 PRELIMINARY; PRT; 11 AA.  
AC Q9G2N4;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Chlamydosaurus kingii (Frisled lizard).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
OC Chlamydosaurus.

OX NCBI\_TaxID=103699;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128469; AAG00644.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1374 MW; A8F73710D3640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

# RESULT 69

## Q8WER7

ID Q8WER7 PRELIMINARY; PRT; 11 AA.  
 AC Q8WER7;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Ceratophora tennentii.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
 OC Ceratophora.  
 OX NCBI\_TaxID=118087;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and phylogenetic information content of mitochondrial  
 RT genomic structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21655505; PubMed=11796034;  
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;

RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora  
 RT Endemic to Sri Lanka.";  
 RL Mol. Phylogenet. Evol. 22:111-117(2002).  
 DR EMBL; AF128521; AAL67607.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 5 AR 6

# RESULT 70

Q8WD50

ID Q8WD50 PRELIMINARY; PRT; 11 AA.  
 AC Q8WD50;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Ceratophora stoddartii.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
 OC Ceratophora.  
 OX NCBI\_TaxID=118196;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21655505; PubMed=11796034;  
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;  
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora  
 RT Endemic to Sri Lanka.";  
 RL Mol. Phylogenet. Evol. 22:111-117(2002).  
 DR EMBL; AF364053; AAL68024.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
 ||  
 Db 5 AR 6

# RESULT 71

Q8SKQ1

ID Q8SKQ1 PRELIMINARY; PRT; 11 AA.  
AC Q8SKQ1;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Ctenophorus cristatus (Crested dragon).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
OC Ctenophorus.  
OX NCBI\_TaxID=180907;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21623804; PubMed=11754013;  
RA Melville J., Schulte J.A. II, Larson A.;  
RT "A molecular phylogenetic study of ecological diversification in the  
RT Australian lizard genus Ctenophorus.";  
RL J. Exp. Zool. 291:339-353(2001).  
DR EMBL; AF375622; AAL78788.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1374 MW; A8F73710D3640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

# RESULT 72

O79639

ID O79639 PRELIMINARY; PRT; 11 AA.  
AC O79639;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Laudakia lehmanni.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
OC Laudakia.  
OX NCBI\_TaxID=71148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98424476; PubMed=9751922;  
RA Macey J.R., Schulte J.A. II, Ananjeva N.B., Larson A.,  
RA Rastegar-Pouyani N., Shammakov S.M., Papenfuss T.J.;  
RT "Phylogenetic relationships among Agamid lizards of the Laudakia  
RT caucasia species group: testing hypotheses of biogeographic

RT fragmentation and an area cladogram for the Iranian Plateau.";  
 RL Mol. Phylogenet. Evol. 10:118-131(1998).  
 DR EMBL; AF028677; AAC99584.1; -.  
 DR PIR; T12244; T12244.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1327 MW; A8F7371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

# RESULT 73

Q9G676

ID Q9G676 PRELIMINARY; PRT; 11 AA.  
 AC Q9G676;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN COI.  
 OS Amphibolurus muricatus (Jacky dragon).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;  
 OC Amphibolurus.  
 OX NCBI\_TaxID=116113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards."  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics."  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128468; AAG00641.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1340 MW; A8F7371E33640446 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

RESULT 74

Q35374

ID Q35374 PRELIMINARY; PRT; 11 AA.  
AC Q35374;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE P1 protein (Fragment).  
OS Paramecium tetraurelia.  
OG Mitochondrion.  
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;  
OC Paramecium.  
OX NCBI\_TaxID=5888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=stock 172;  
RX MEDLINE=87055241; PubMed=3023187;  
RA Pritchard A.E., Seilhamer J.J., Cummings D.J.;  
RT "Paramecium mitochondrial DNA sequences and RNA transcripts for  
RT cytochrome oxidase subunit I, URFl, and three ORFs adjacent to the  
RT replication origin."  
RL Gene 44:243-253(1986).  
DR EMBL; M15280; AAA79267.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1266 MW; 1D84259D16D046D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 RS 11  
||  
Db 8 RS 9

RESULT 75

Q9G5V0

ID Q9G5V0 PRELIMINARY; PRT; 11 AA.  
AC Q9G5V0;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN COI.  
OS Laudakia stoliczkana.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;  
OC Laudakia.



OX NCBI\_TaxID=118214;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114082; PubMed=12118408;  
 RA Macey J.R., Schulte J.A. II, Larson A.;  
 RT "Evolution and information content of the mitochondrial genomic  
 RT structural features illustrated with acrodont lizards.";  
 RL Syst. Biol. 49:257-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22114081; PubMed=12118407;  
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard  
 RT phylogenetics.";  
 RL Syst. Biol. 49:233-256(2000).  
 DR EMBL; AF128519; AAG00794.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1327 MW; A8F7371E336411A6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
 ||  
 Db 3 TM 4

Search completed: April 8, 2004, 15:46:06  
 Job time : 28.7692 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds  
 (without alignments)  
 111.135 Million cell updates/sec

Title: US-09-787-443A-12  
 Perfect score: 11  
 Sequence: 1 ARQKTMKPRRS 11

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11

Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length	Length			
1	3	27.3	11	1	Q20A	COMTE	P80464 comamonas t
2	3	27.3	11	1	TKNA	GADMO	P28498 gadus morhu
3	3	27.3	11	1	TKNA	ONCMY	P28499 oncorhynchu
4	3	27.3	11	1	TKNA	SCYCA	P41333 scyliorhinu
5	2	18.2	11	1	BPP3	BOTIN	P30423 bothrops in
6	2	18.2	11	1	BPP4	BOTIN	P30424 bothrops in
7	2	18.2	11	1	BPPB	AGKHA	P01021 agkistrodon
8	2	18.2	11	1	CSI5	BACSU	P81095 bacillus su
9	2	18.2	11	1	ES1	RAT	P56571 rattus norv
10	2	18.2	11	1	MHBI	KLEPN	P80580 klebsiella
11	2	18.2	11	1	OAIF	SARBU	P83518 sarcophaga
12	2	18.2	11	1	PKC1	CARMO	P82684 carausius m
13	2	18.2	11	1	RR2	CONAM	P42341 conopholis
14	2	18.2	11	1	RS30	ONCMY	P83328 oncorhynchu
15	2	18.2	11	1	TIN1	HOPTI	P82651 hoplobatrach
16	2	18.2	11	1	TKN2	UPERU	P08616 uperoleia r
17	2	18.2	11	1	TKNA	CHICK	P19850 gallus gall

18	2	18.2	11	1	TKNA_HORSE	P01290	equus cabal
19	2	18.2	11	1	TKNA_RANCA	P22688	rana catesb
20	2	18.2	11	1	TKNA_RANRI	P29207	rana ridibu
21	2	18.2	11	1	TKND_RANCA	P22691	rana catesb
22	2	18.2	11	1	UXB2_YEAST	P99013	saccharomyc
23	1	9.1	11	1	ANGT_CRIGE	P09037	crinia geor
24	1	9.1	11	1	ASL1_BACSE	P83146	bacteroides
25	1	9.1	11	1	ASL2_BACSE	P83147	bacteroides
26	1	9.1	11	1	BPP_AGKHP	P04562	agkistrodon
27	1	9.1	11	1	BRK_MEGFL	P12797	megascolia
28	1	9.1	11	1	CA21_LITCI	P82087	litoria cit
29	1	9.1	11	1	CA22_LITCI	P82088	litoria cit
30	1	9.1	11	1	CA31_LITCI	P82089	litoria cit
31	1	9.1	11	1	CA32_LITCI	P82090	litoria cit
32	1	9.1	11	1	CA41_LITCI	P82091	litoria cit
33	1	9.1	11	1	CA42_LITCI	P82092	litoria cit
34	1	9.1	11	1	CEP1_ACHFU	P22790	achatina fu
35	1	9.1	11	1	CORZ_PERAM	P11496	periplaneta
36	1	9.1	11	1	COXA_CANFA	P99501	canis famil
37	1	9.1	11	1	CX5A_CONAL	P58848	conus aulic
38	1	9.1	11	1	CX5B_CONAL	P58849	conus aulic
39	1	9.1	11	1	CXL1_CONMR	P58807	conus marmo
40	1	9.1	11	1	EFG_CLOPA	P81350	clostridium
41	1	9.1	11	1	FAR6_PENMO	P83321	penaeus mon
42	1	9.1	11	1	FAR9_CALVO	P41864	calliphora
43	1	9.1	11	1	HS70_PINPS	P81672	pinus pinas
44	1	9.1	11	1	LADD_ONCMY	P81018	oncorhynch
45	1	9.1	11	1	LPW_THETH	P05624	thermus the
46	1	9.1	11	1	LSK1_LEUMA	P04428	leucophaea
47	1	9.1	11	1	LSKP_PERAM	P36885	periplaneta
48	1	9.1	11	1	MLG_THETS	P41989	theromyzon
49	1	9.1	11	1	MORN_HUMAN	P01163	homo sapien
50	1	9.1	11	1	NUHM_CANFA	P49820	canis famil
51	1	9.1	11	1	NXSN_PSETE	P59072	pseudonaja
52	1	9.1	11	1	PQQC_PSEFL	P55173	pseudomonas
53	1	9.1	11	1	PVK1_PERAM	P41837	periplaneta
54	1	9.1	11	1	RANC_RANPI	P08951	rana pipien
55	1	9.1	11	1	RRPL_CHAV	P13179	chandipura
56	1	9.1	11	1	T2P1_PROVU	P31031	proteus vul
57	1	9.1	11	1	TIN4_HOPTI	P82654	hoplobatrac
58	1	9.1	11	1	TKC2_CALVO	P41518	calliphora
59	1	9.1	11	1	TKN1_PSEGU	P42986	pseudophryn
60	1	9.1	11	1	TKN1_UPEIN	P82026	uperoleia i
61	1	9.1	11	1	TKN1_UPERU	P08612	uperoleia r
62	1	9.1	11	1	TKN2_PSEGU	P42987	pseudophryn
63	1	9.1	11	1	TKN3_PSEGU	P42988	pseudophryn
64	1	9.1	11	1	TKN4_PSEGU	P42989	pseudophryn
65	1	9.1	11	1	TKN5_PSEGU	P42990	pseudophryn
66	1	9.1	11	1	TKN_ELEMO	P01293	eledone mos
67	1	9.1	11	1	TKN_PHYFU	P08615	physalaemus
68	1	9.1	11	1	UF05_MOUSE	P38643	mus musculu
69	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapien
70	0	0.0	11	1	RE41_LITRU	P82074	litoria rub

# ALIGNMENTS

# RESULT 1

## Q20A\_COMTE

ID Q20A\_COMTE STANDARD; PRT; 11 AA.  
AC P80464;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).  
OS Comamonas testosteroni (Pseudomonas testosteroni).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Comamonadaceae; Comamonas.  
OX NCBI\_TaxID=285;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=63;  
RX MEDLINE=96035889; PubMed=7556204;  
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;  
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-  
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
RT quinoline and 3-methylquinoline degradation.";  
RL Eur. J. Biochem. 232:536-544(1995).  
CC -!- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)-2-oxo-  
CC 1,2-dihydroquinoline.  
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-  
CC 1(2H)-one + reduced acceptor.  
CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.  
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first  
CC step.  
CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and  
CC two gamma chains (Probable).  
DR PIR; S66606; S66606.  
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9  
| | |  
Db 9 KPR 11

# RESULT 2

## TKNA\_GADMO

ID TKNA\_GADMO STANDARD; PRT; 11 AA.  
AC P28498;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
OS Gadus morhua (Atlantic cod).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.

OX NCBI\_TaxID=8049;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout."  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S23306; S23306.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
 |||  
 Db 1 KPR 3

### RESULT 3

#### TKNA\_ONCMY

ID TKNA\_ONCMY STANDARD; PRT; 11 AA.  
 AC P28499;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout."  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and

CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S23308; S23308.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION (BY SIMILARITY).  
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
 |||  
 Db 1 KPR 3

#### RESULT 4

TKNA\_SCYCA  
 ID TKNA\_SCYCA STANDARD; PRT; 11 AA.  
 AC P41333;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; Scyliorhinus.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=93292508; PubMed=7685693;  
 RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;  
 RT "Primary structures and biological activities of substance-P-related  
 RT peptides from the brain of the dogfish, Scyliorhinus canicula.";  
 RL Eur. J. Biochem. 214:469-474(1993).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; S33300; S33300.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KPR 9  
|||  
Db 1 KPR 3

RESULT 5

BPP3\_BOTIN

ID BPP3\_BOTIN STANDARD; PRT; 11 AA.  
AC P30423;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting  
DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom."  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; C37196; C37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
||  
Db 5 PR 6

RESULT 6

BPP4\_BOTIN

ID BPP4\_BOTIN STANDARD; PRT; 11 AA.  
AC P30424;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting

DE enzyme inhibitor).

OS Bothrops insularis (Island jararaca) (Queimada jararaca).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Bothrops.

OX NCBI\_TaxID=8723;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating

RT peptides from Bothrops insularis snake venom.";

RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.

DR PIR; D37196; D37196.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9

||

Db 5 PR 6

#### RESULT 7

BPPB\_AGKHA

ID BPPB\_AGKHA STANDARD; PRT; 11 AA.

AC P01021;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide B (Angiotensin-converting

DE enzyme inhibitor).

OS Agkistrodon halys blomhoffii (Mamushi) (Gloydus blomhoffii).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Gloydus.

OX NCBI\_TaxID=242054;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RA Kato H., Suzuki T.;

RT "Amino acid sequence of bradykinin-potentiating peptide isolated from

RT the venom of Agkistrodon halys blomhoffii.";

RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).

CC -!- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.



DR PIR; A01254; XASNBA.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PR 9  
||  
Db 5 PR 6

#### RESULT 8

CSI5\_BACSU  
ID CSI5\_BACSU STANDARD; PRT; 11 AA.  
AC P81095;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=168 / JH642;  
RA Graumann P.L., Schmid R., Marahiel M.A.;  
RL Submitted (OCT-1997) to Swiss-Prot.  
RN [2]  
RP CHARACTERIZATION.  
RC STRAIN=168 / JH642;  
RX MEDLINE=96345629; PubMed=8755892;  
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;  
RT "Cold shock stress-induced proteins in Bacillus subtilis."  
RL J. Bacteriol. 178:4611-4619(1996).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- INDUCTION: In response to low temperature.  
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KP 8  
||  
Db 7 KP 8

#### RESULT 9

ES1\_RAT  
ID ES1\_RAT STANDARD; PRT; 11 AA.  
AC P56571;  
DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE ES1 protein, mitochondrial (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to Swiss-Prot.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).  
 CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot  
 CC P2) is: 8.9, its MW is: 25 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2  
 ||  
 Db 2 AR 3

#### RESULT 10

MHBI\_KLEPN  
 ID MHBI\_KLEPN STANDARD; PRT; 11 AA.  
 AC P80580;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).  
 GN MHBI.  
 OS Klebsiella pneumoniae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=573;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96349117; PubMed=8760924;  
 RA Robson N.D., Parrott S., Cooper R.A.;  
 RT "In vitro formation of a catabolic plasmid carrying Klebsiella  
 RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-  
 RT hydroxybenzoate."  
 RL Microbiology 142:2115-2120(1996).  
 CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.  
 KW Isomerase.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MK 7  
||  
Db 1 MK 2

RESULT 11

OAIF\_SARBU

ID OAIF\_SARBU STANDARD; PRT; 11 AA.  
AC P83518;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-ODAIF(1-9); Neb-ODAIF(1-7)].  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.  
RC TISSUE=Ovary;  
RX MEDLINE=22272747; PubMed=12383874;  
RA Vandingenen A., Hens K., Baggerman G., Macours N., Schoofs L.,  
RA De Loof A., Huybrechts R.;  
RT "Isolation and characterization of an angiotensin converting enzyme  
RT substrate from vitellogenic ovaries of Neobellieria bullata.";  
RL Peptides 23:1853-1863(2002).  
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in  
CC vitro.  
CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-  
CC terminal dipeptides.  
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.  
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.  
FT PEPTIDE 1 11 NEB-ODAIF.  
FT PEPTIDE 1 9 NEB-ODAIF(1-9).  
FT PEPTIDE 1 7 NEB-ODAIF(1-7).  
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KP 8  
||  
Db 4 KP 5

RESULT 12

PKC1\_CARMO

ID PKC1\_CARMO STANDARD; PRT; 11 AA.  
AC P82684;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).  
 OS Carausius morosus (Indian stick insect).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;  
 OC Heteronemiidae; Carausius.  
 OX NCBI\_TaxID=7022;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RA Predel R., Kellner R., Gaede G.;  
 RT "Myotropic neuropeptides from the retrocerebral complex of the stick  
 RT insect, Carausius morosus (Phasmatodea: Lonchodidae).";  
 RL Eur. J. Entomol. 96:275-278(1999).  
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
 CC activity).  
 CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.  
 CC -!- SIMILARITY: Belongs to the pyrokinin family.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
 ||  
 Db 9 PR 10

# RESULT 13

## RR2\_CONAM

ID RR2\_CONAM STANDARD; PRT; 11 AA.  
 AC P42341;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S2 (Fragment).  
 GN RPS2.  
 OS Conopholis americana (Squawroot).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamiids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.  
 OX NCBI\_TaxID=4179;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92145776; PubMed=1723664;  
 RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;  
 RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss  
 RT of photosynthesis in a lineage of parasitic plants.";  
 RL Curr. Genet. 20:515-518(1991).  
 CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.  
 CC -----

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CC -----

DR EMBL; X64567; CAA45868.1; -.  
DR PIR; S32575; S32575.  
DR HAMAP; MF\_00291; -; 1.  
DR InterPro; IPR001865; Ribosomal\_S2.  
DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; PARTIAL.  
DR PROSITE; PS00963; RIBOSOMAL\_S2\_2; PARTIAL.  
KW Ribosomal protein; Chloroplast.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RR 10  
||  
Db 3 RR 4

#### RESULT 14

##### RS30\_ONCMY

ID RS30\_ONCMY STANDARD; PRT; 11 AA.  
AC P83328;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE 40S ribosomal protein S30 (Fragment).  
GN FAU.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Skin mucus;  
RX MEDLINE=22142142; PubMed=12147245;  
RA Fernandes J.M.O., Smith V.J.;  
RT "A novel antimicrobial function for a ribosomal peptide from rainbow  
RT trout skin.";  
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).  
CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
CC bacteria.  
CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.  
CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.  
KW Ribosomal protein; Antibiotic.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AR 2  
||  
Db 7 AR 8

RESULT 15

TIN1\_HOPTI

ID TIN1\_HOPTI STANDARD; PRT; 11 AA.  
AC P82651;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tigerinin-1.  
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC Hoplobatrachus.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;  
RX PubMed=11031261;  
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
RA Devi A.S., Nagaraj R., Sitaram N.;  
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
RT tigerina.";  
RL J. Biol. Chem. 276:2701-2707(2001).  
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,  
CC S.aureus, M.luteus, P.putida and S.cerevisiae.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.  
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.  
FT DISULFID 2 10  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TM 6  
||  
Db 3 TM 4

RESULT 16

TKN2\_UPERU

ID TKN2\_UPERU STANDARD; PRT; 11 AA.  
AC P08616;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Rugosauperolein II ([Lys5,Thr6]physalaemin).  
 OS Uperoleia rugosa (Wrinkled toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=8368;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=80223080; PubMed=7389029;  
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;  
 RT "Physalaemin- and bombesin-like peptides in the skin of the  
 RT Australian leptodactylid frog Uperoleia rugosa."  
 RL Chem. Pharm. Bull. 28:689-695(1980).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KT 5  
 ||  
 Db 5 KT 6

#### RESULT 17

##### TKNA\_CHICK

ID TKNA\_CHICK STANDARD; PRT; 11 AA.  
 AC P19850;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=88204263; PubMed=2452461;  
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;

RT "[Arg3]substance P and neurokinin A from chicken small intestine.";  
 RL Regul. Pept. 20:171-180(1988).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; JN0023; JN0023.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PR 9  
 ||  
 Db 2 PR 3

# RESULT 18

## TKNA\_HORSE

ID TKNA\_HORSE STANDARD; PRT; 11 AA.  
 AC P01290;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 GN TAC1 OR NKNA OR TAC2 OR NKA.  
 OS Equus caballus (Horse), and  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796, 10141;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Horse;  
 RA Studer R.O., Trzeciak A., Lergier W.;  
 RT "Isolation and amino-acid sequence of substance P from horse  
 RT intestine.";  
 RL Helv. Chim. Acta 56:860-866(1973).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=C.porcellus;  
 RX MEDLINE=90044685; PubMed=2478925;  
 RA Murphy R.;  
 RT "Primary amino acid sequence of guinea-pig substance P.";  
 RL Neuropeptides 14:105-110(1989).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.



CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A01558; SPHO.  
 DR PIR; A60654; A60654.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
 ||  
 Db 3 KP 4

# RESULT 19

TKNA\_RANCA  
 ID TKNA\_RANCA STANDARD; PRT; 11 AA.  
 AC P22688;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranatachykinin A (RTK A).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain, and Intestine;  
 RX MEDLINE=91254337; PubMed=2043143;  
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
 RT brain and intestine.";  
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=94023216; PubMed=8210506;  
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
 RT intestine.";  
 RL Regul. Pept. 46:81-88(1993).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A61033; A61033.

DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
 ||  
 Db 1 KP 2

# RESULT 20

## TKNA\_RANRI

ID TKNA\_RANRI STANDARD; PRT; 11 AA.  
 AC P29207;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranakinin (Substance-P-related peptide).  
 OS Rana ridibunda (Laughing frog) (Marsh frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8406;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=92044543; PubMed=1658233;  
 RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;  
 RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with  
 RT neurokinin B from the brain of the frog Rana ridibunda."  
 RL J. Neurochem. 57:2086-2091(1991).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
||  
Db 1 KP 2

RESULT 21

TKND\_RANCA

ID TKND\_RANCA STANDARD; PRT; 11 AA.  
AC P22691;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ranatachykinin D (RTK D).  
OS Rana catesbeiana (Bull frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8400;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Intestine;  
RX MEDLINE=91254337; PubMed=2043143;  
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;  
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)  
RT brain and intestine.";  
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=94023216; PubMed=8210506;  
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;  
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and  
RT intestine.";  
RL Regul. Pept. 46:81-88(1993).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; D61033; D61033.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR PROSITE; PS00267; TACHYKININ; FALSE\_NEG.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KP 8  
||  
Db 1 KP 2

RESULT 22

UXB2\_YEAST

ID UXB2\_YEAST STANDARD; PRT; 11 AA.  
AC P99013;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=X2180-1A;  
RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,  
RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;  
RL Submitted (AUG-1995) to Swiss-Prot.  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 6.20, its MW is: 9.2 kDa.  
DR SWISS-2DPAGE; P99013; YEAST.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2  
||  
Db 7 AR 8

# RESULT 23

## ANGT\_CRIGE

ID ANGT\_CRIGE STANDARD; PRT; 11 AA.  
AC P09037;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Crinia-angiotensin II.  
OS Crinia georgiana (Quacking frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
OC Myobatrachinae; Crinia.  
OX NCBI\_TaxID=8374;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=80024575; PubMed=488254;  
RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;  
RT "Amino acid composition and sequence of crinia-angiotensin, an  
RT angiotensin II-like endecapeptide from the skin of the Australian  
RT frog Crinia georgiana."  
RL Experientia 35:1132-1133(1979).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
DR PIR; S07207; S07207.  
KW Vasoconstrictor.

SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 1 A 1

RESULT 24

ASL1\_BACSE

ID ASL1\_BACSE STANDARD; PRT; 11 AA.  
AC P83146;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).  
OS Bacteroides stercoris.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=46506;  
RN [1]  
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.  
RC STRAIN=HJ-15;  
RX MEDLINE=21223019; PubMed=11322884;  
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;  
RT "Purification and characterization of acharan sulfate lyases, two  
RT novel heparinases, from Bacteroides stercoris HJ-15.";  
RL Eur. J. Biochem. 268:2635-2641(2001).  
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,  
CC heparin and heparan sulfate.  
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.  
CC Activated by reducing agents, such as DL-dithiothreitol and 2-  
CC mercaptoethanol.  
CC -!- SUBUNIT: Monomer.  
CC -!- PTM: The N-terminus is blocked.  
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is  
CC 7.2 and optimum temperature 45 degrees Celsius.  
KW Lyase; Heparin-binding.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 11 Q 11

RESULT 25

ASL2\_BACSE

ID ASL2\_BACSE STANDARD; PRT; 11 AA.

AC P83147;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).  
 OS Bacteroides stercoris.  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Bacteroidaceae; Bacteroides.  
 OX NCBI\_TaxID=46506;  
 RN [1]  
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.  
 RC STRAIN=HJ-15;  
 RX MEDLINE=21223019; PubMed=11322884;  
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;  
 RT "Purification and characterization of acharan sulfate lyases, two  
 RT novel heparinases, from Bacteroides stercoris HJ-15.";  
 RL Eur. J. Biochem. 268:2635-2641(2001).  
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,  
 CC heparin and heparan sulfate.  
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.  
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-  
 CC mercaptoethanol.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- PTM: The N-terminus is blocked.  
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is  
 CC 7.2 and optimum temperature 45 degrees Celsius.  
 KW Lyase; Heparin-binding.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 T 5  
 |  
 Db 1 T 1

#### RESULT 26

##### BPP\_AGKHP

ID BPP\_AGKHP STANDARD; PRT; 11 AA.  
 AC P04562;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydus halys  
 OS pallas).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Gloydus.  
 OX NCBI\_TaxID=8714;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Venom;  
RX MEDLINE=86177022; PubMed=3008123;  
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;  
RT "Structure-function studies on the bradykinin potentiating peptide  
RT from Chinese snake venom (*Agkistrodon halys pallas*).";  
RL Peptides 6 Suppl. 3:339-342(1985).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; JC0002; XAVIBH.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

# RESULT 27

BRK\_MEGFL  
ID BRK\_MEGFL STANDARD; PRT; 11 AA.  
AC P12797;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like  
DE peptide ([Thr6]bradykinin)].  
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Scoliidae; Megascolia.  
OX NCBI\_TaxID=7437;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=87293024; PubMed=3617088;  
RA Yasuhara T., Mantel P., Nakajima T., Piek T.;  
RT "Two kinins isolated from an extract of the venom reservoirs of the  
RT solitary wasp *Megascolia flavifrons*.";  
RL Toxicon 25:527-535(1987).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RA Nakajima T., Piek T., Yashuara T., Mantel P.;  
RT "Two kinins isolated from the venom of *Megascolia flavifrons*.";  
RL Toxicon 26:34-34(1988).  
CC -!- FUNCTION: Both proteins have bradykinin-like, although lower  
CC activities (e.g. smooth muscle contraction).  
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.  
CC -!- SIMILARITY: Belongs to the bradykinin family.  
DR PIR; B26744; B26744.

DR GO; GO:0005615; C:extracellular space; IDA.  
 DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.  
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.  
 KW Bradykinin; Vasodilator.  
 FT PEPTIDE 1 11 MEGASCOLIAKININ.  
 FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.  
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
 |  
 Db 1 R 1

# RESULT 28

CA21\_LITCI

ID CA21\_LITCI STANDARD; PRT; 11 AA.  
 AC P82087;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 2.1/2.1Y4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;



Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

# RESULT 29

CA22\_LITCI

ID CA22\_LITCI STANDARD; PRT; 11 AA.  
AC P82088;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Caerulein 2.2/2.2Y4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylinae;  
OC Pelodytidae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=20057701; PubMed=10589099;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
RT "Caerulein-like peptides from the skin glands of the Australian blue  
RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
RT using electrospray mass spectrometry."  
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being  
CC sulfated.  
CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

# RESULT 30

CA31\_LITCI

ID CA31\_LITCI STANDARD; PRT; 11 AA.

AC P82089;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 3.1/3.1Y4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

# RESULT 31

## CA32\_LITCI

ID CA32\_LITCI STANDARD; PRT; 11 AA.

AC P82090;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein 3.2/3.2Y4.

OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

OC Pelodyadinae; Litoria.

OX NCBI\_TaxID=94770;

RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT montains tree frog *Litoria citropa*. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

# RESULT 32

## CA41\_LITCI

ID CA41\_LITCI STANDARD; PRT; 11 AA.  
 AC P82091;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 4.1/4.1Y4.  
 OS *Litoria citropa* (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodyadinae; *Litoria*.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT montains tree frog *Litoria citropa*. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).

CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 4 4 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

# RESULT 33

CA42\_LITCI  
 ID CA42\_LITCI STANDARD; PRT; 11 AA.  
 AC P82092;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Caerulein 4.2/4.2Y4.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20057701; PubMed=10589099;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;  
 RT "Caerulein-like peptides from the skin glands of the Australian blue  
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination  
 RT using electrospray mass spectrometry."  
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).  
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being  
 CC sulfated.  
 CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; FALSE\_NEG.  
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;  
 KW Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 4 4 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

#### RESULT 34

CEP1\_ACHFU  
ID CEP1\_ACHFU STANDARD; PRT; 11 AA.  
AC P22790;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Cardio-excitatory peptide-1 (ACEP-1).  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Ferussac; TISSUE=Heart atrium;  
RX MEDLINE=90211261; PubMed=2322251;  
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;  
RT "A novel cardio-excitatory peptide isolated from the atria of the  
RT African giant snail, Achatina fulica."  
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).  
CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also  
CC excitatory actions on the penis retractor muscle, the buccal  
CC muscle and the identified neurons controlling the buccal muscle  
CC movement of achatina.  
CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.  
DR PIR; A34662; A34662.  
KW Hormone; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 3 Q 3

#### RESULT 35

CORZ\_PERAM  
ID CORZ\_PERAM STANDARD; PRT; 11 AA.  
AC P11496;

DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Corazonin.  
 OS *Periplaneta americana* (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; *Periplaneta*.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=89325572; PubMed=2753132;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of corazonin, a cardioactive peptide from  
 RT the American cockroach.";  
 RL FEBS Lett. 250:231-234(1989).  
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved  
 CC in the physiological regulation of the heart beat.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 DR PIR; S05002; S05002.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

# RESULT 36

COXA\_CANFA  
 ID COXA\_CANFA STANDARD; PRT; 11 AA.  
 AC P99501;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).  
 GN COX5A.  
 OS *Canis familiaris* (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; *Canis*.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c

CC oxidase, the terminal oxidase in mitochondrial electron transport.  
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.  
 DR HSC-2DPAGE; P99501; DOG.  
 DR InterPro; IPR003204; Cyt\_c\_ox5A.  
 DR Pfam; PF02284; COX5A; 1.  
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 T 5  
 |  
 Db 7 T 7

# RESULT 37

## CX5A\_CONAL

ID CX5A\_CONAL STANDARD; PRT; 11 AA.  
 AC P58848;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Conotoxin au5a.  
 OS Conus aulicus (Court cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99452958; PubMed=10521453;  
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
 RT "The T-superfamily of conotoxins."  
 RL J. Biol. Chem. 274:30664-30671(1999).  
 RN [2]  
 RP ERRATUM.  
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
 RL J. Biol. Chem. 274:36030-36030(1999).  
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is  
 CC observed when injected into mice.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.  
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.  
 DR PIR; A59146; A59146.  
 KW Toxin.

FT DISULFID 2 9  
FT DISULFID 3 10  
SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 7 R 7

#### RESULT 38

##### CX5B\_CONAL

ID CX5B\_CONAL STANDARD; PRT; 11 AA.  
AC P58849;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Conotoxin au5b.  
OS Conus aulicus (Court cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=89437;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99452958; PubMed=10521453;  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RT "The T-superfamily of conotoxins."  
RL J. Biol. Chem. 274:30664-30671(1999).  
RN [2]  
RP ERRATUM.  
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,  
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,  
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;  
RL J. Biol. Chem. 274:36030-36030(1999).  
CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is  
CC observed when injected into mice (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.  
CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.  
DR PIR; B59146; B59146.  
KW Toxin.  
FT DISULFID 2 9  
FT DISULFID 3 10  
SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 2 R 2  
|  
Db 7 R 7

RESULT 39

CXL1\_CONMR

ID CXL1\_CONMR STANDARD; PRT; 11 AA.  
AC P58807;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Lambda-conotoxin CMrVIA.  
OS Conus marmoreus (Marble cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=42752;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=20564325; PubMed=10988292;  
RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
RA Seow K.T., Bay B.-H.;  
RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide  
RT pattern and protein folding. Isolation and characterization from the  
RT venom of Conus marmoreus.";  
RL J. Biol. Chem. 275:39516-39522(2000).  
CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=1237.93; MW\_ERR=0.21; METHOD=Electrospray.  
CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.  
KW Neurotoxin; Toxin; Hydroxylation.  
FT DISULFID 2 11  
FT DISULFID 3 8  
FT MOD\_RES 10 10 HYDROXYLATION.  
SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 K 4  
|  
Db 6 K 6

RESULT 40

EFG\_CLOPA

ID EFG\_CLOPA STANDARD; PRT; 11 AA.  
AC P81350;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Elongation factor G (EF-G) (CP 5) (Fragment).  
GN FUSA.

OS *Clostridium pasteurianum*.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC *Clostridium*.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flengsrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from *Clostridium pasteurianum* W5.";  
 RL Electrophoresis 19:802-806(1998).  
 CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of  
 CC the nascent protein chain from the A-site to the P-site of the  
 CC ribosome.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.  
 CC EF-G/EF-2 subfamily.  
 DR InterPro; IPR000795; EF\_GTPbind.  
 DR PROSITE; PS00301; EFACTOR\_GTP; PARTIAL.  
 KW Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 K 4  
 |  
 Db 1 K 1

#### RESULT 41

##### FAR6\_PENMO

ID FAR6\_PENMO STANDARD; PRT; 11 AA.  
 AC P83321;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).  
 OS *Penaeus monodon* (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; *Penaeus*.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn *Penaeus monodon*.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.

CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 3 R 3

#### RESULT 42

FAR9\_CALVO

ID FAR9\_CALVO STANDARD; PRT; 11 AA.  
AC P41864;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CalliFMRFamide 9.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliFMRFamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
CC family.  
DR PIR; I41978; I41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
|  
Db 10 R 10

#### RESULT 43

HS70\_PINPS

ID HS70\_PINPS STANDARD; PRT; 11 AA.  
AC P81672;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Heat shock 70 kDa protein (Fragment).  
OS Pinus pinaster (Maritime pine).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
OX NCBI\_TaxID=71647;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Needle;  
RX MEDLINE=99274088; PubMed=10344291;  
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
RA Frigerio J.-M., Plomion C.;  
RT "Separation and characterization of needle and xylem maritime pine  
RT proteins.";  
RL Electrophoresis 20:1098-1108(1999).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein  
CC (spot N164) is: 5.4, its MW is: 73 kDa.  
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.  
KW ATP-binding; Heat shock; Multigene family.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1  
|  
Db 5 A 5

#### RESULT 44

##### LADD\_ONCMY

ID LADD\_ONCMY STANDARD; PRT; 11 AA.  
AC P81018;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Ladderlectin (Fragment).  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Blood;  
RX MEDLINE=97293418; PubMed=9149391;  
RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;  
RT "A rainbow trout lectin with multimeric structure.";  
RL Comp. Biochem. Physiol. 116B:385-390(1997).  
CC -!- FUNCTION: Lectin that binds sepharose.

CC -!- COFACTOR: Calcium is essential for sepharose binding.  
 CC -!- SUBUNIT: Multimeric.  
 KW Lectin; Calcium.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 1 A 1

# RESULT 45

LPW\_THETH

ID LPW\_THETH STANDARD; PRT; 11 AA.  
 AC P05624;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Trp operon leader peptide.  
 GN TRPL.  
 OS Thermus thermophilus.  
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
 OC Thermus.  
 OX NCBI\_TaxID=274;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HB8 / ATCC 27634;  
 RX MEDLINE=89000781; PubMed=2844259;  
 RA Sato S., Nakada Y., Kanaya S., Tanaka T.;  
 RT "Molecular cloning and nucleotide sequence of Thermus thermophilus  
 RT HB8 trpE and trpG."  
 RL Biochim. Biophys. Acta 950:303-312(1988).  
 CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS  
 CC OF TRYPTOPHAN.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

DR EMBL; X07744; CAA30565.1; -.  
 KW Tryptophan biosynthesis; Leader peptide.  
 SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 M 6  
 |

Db

1 M 1

RESULT 46

LSK1\_LEUMA

ID LSK1\_LEUMA STANDARD; PRT; 11 AA.  
AC P04428;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Leucosulfakinin-I (LSK-I).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86315858; PubMed=3749893;  
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;  
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to  
RT gastrin and cholecystokinin."  
RL Science 234:71-73(1986).  
CC -!- FUNCTION: Change the frequency and amplitude of contractions of  
CC the hingat. Inhibits muscle contraction of hindgut.  
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
DR PIR; A01622; GMROL.  
DR InterPro; IPR001651; Gastrin.  
DR PROSITE; PS00259; GASTRIN; 1.  
KW Hormone; Amidation; Sulfation.  
FT MOD\_RES 6 6 SULFATION.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 2 Q 2

RESULT 47

LSKP\_PERAM

ID LSKP\_PERAM STANDARD; PRT; 11 AA.  
AC P36885;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Perisulfakinin (Pea-SK-I).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]

RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90137190; PubMed=2615921;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from  
 RT the American cockroach homologous to the leucosulfakinins."  
 RL Neuropeptides 14:145-149(1989).  
 CC -!- FUNCTION: Stimulates hindgut contractions.  
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR PIR; A60656; A60656.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KW Hormone; Amidation; Sulfation.  
 FT MOD\_RES 6 6 SULFATION.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 2 Q 2

#### RESULT 48

##### MLG\_THETS

ID MLG\_THETS STANDARD; PRT; 11 AA.  
 AC P41989;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).  
 OS Theromyzon tessulatum (Leech).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.  
 OX NCBI\_TaxID=13286;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=94298944; PubMed=8026574;  
 RA Salzet M., Wattez C., Bulet P., Malecha J.;  
 RT "Isolation and structural characterization of a novel peptide related  
 RT to gamma-melanocyte stimulating hormone from the brain of the leech  
 RT Theromyzon tessulatum."  
 RL FEBS Lett. 348:102-106(1994).  
 CC -!- SIMILARITY: Belongs to the POMC family.  
 DR PIR; S45698; S45698.  
 KW Hormone; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           6 M 6  
              |  
Db           3 M 3

RESULT 49

MORN\_HUMAN

ID MORN\_HUMAN       STANDARD;       PRT;    11 AA.  
AC P01163;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Morphogenetic neuropeptide (Head activator) (HA).  
OS Homo sapiens (Human),  
OS Rattus norvegicus (Rat),  
OS Bos taurus (Bovine),  
OS Anthopleura elegantissima (Sea anemone), and  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Human, Rat, and Bovine;  
RX MEDLINE=82035850; PubMed=7290191;  
RA Bodenmuller H., Schaller H.C.;  
RT "Conserved amino acid sequence of a neuropeptide, the head activator,  
RT from coelenterates to humans."  
RL Nature 293:579-580(1981).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=A.elegantissima, and H.attenuata;  
RA Schaller H.C., Bodenmuller H.;  
RT "Isolation and amino acid sequence of a morphogenetic peptide from  
RT hydra."  
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).  
RN [3]  
RP SYNTHESIS.  
RX MEDLINE=82050803; PubMed=7297679;  
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;  
RT "Synthesis of a new neuropeptide, the head activator from hydra."  
RL FEBS Lett. 131:317-321(1981).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=90059923; PubMed=2583101;  
RA Schaller H.C., Druffel-Augustin S., Dubel S.;  
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells  
RT in the G2/mitosis transition."  
RL EMBO J. 8:3311-3318(1989).  
CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells  
CC       in the G2/mitosis transition.  
CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra  
CC       and was called head activator by the authors, because it induced  
CC       head-specific growth and differentiation in this animal. It has  
CC       been found in mammalian intestine and hypothalamus.  
DR PIR; A01427; YHRT.  
DR PIR; A93900; YHXAE.



DR PIR; B01427; YHHU.  
 DR PIR; B93900; YHJFHY.  
 DR PIR; C01427; YHBO.  
 DR GK; P01163; -.  
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

RESULT 50

NUHM\_CANFA

ID NUHM\_CANFA STANDARD; PRT; 11 AA.  
 AC P49820;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)  
 DE (EC 1.6.99.3) (Fragment).  
 GN NDUFV2.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY  
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED  
 CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)  
 CC FRAGMENT OF THE ENZYME.  
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.  
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).  
 CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.  
 CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the  
 CC mitochondrial inner membrane.  
 CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.  
 DR HSC-2DPAGE; P49820; DOG.  
 DR InterPro; IPR002023; Cmplx1\_24kDa.  
 DR PROSITE; PS01099; COMPLEX1\_24K; PARTIAL.  
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;  
 KW Iron-sulfur; Iron; 2Fe-2S.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
|  
Db 2 A 2

RESULT 51

NXSN\_PSETE

ID NXSN\_PSETE STANDARD; PRT; 11 AA.  
AC P59072;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).  
OS Pseudonaja textilis (Eastern brown snake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Elapidae; Acanthophiinae; Pseudonaja.  
OX NCBI\_TaxID=8673;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=99449602; PubMed=10518793;  
RA Gong N.L., Armugam A., Jeyaseelan K.;  
RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA  
RT cloning, expression and protein characterization.";  
RL Eur. J. Biochem. 265:982-989(1999).  
CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic  
CC acetylcholine receptors (nAChR).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.  
CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.  
CC -!- SIMILARITY: Belongs to the snake toxin family.  
DR InterPro; IPR003571; Snake\_toxin.  
DR PROSITE; PS00272; SNAKE\_TOXIN; PARTIAL.  
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;  
KW Acetylcholine receptor inhibitor; Multigene family.  
FT UNSURE 3 3  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 T 5  
|  
Db 2 T 2

RESULT 52

PQQC\_PSEFL

ID PQQC\_PSEFL STANDARD; PRT; 11 AA.  
AC P55173;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone  
DE biosynthesis protein C) (Fragment).  
GN PQQC.  
OS Pseudomonas fluorescens.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=294;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CHA0;  
RX MEDLINE=96064397; PubMed=8526497;  
RA Schnider U., Keel C., Defago G., Haas D.;  
RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:  
RT mutational inactivation of the genes results in overproduction of the  
RT antibiotic pyoluteorin.";  
RL Appl. Environ. Microbiol. 61:3856-3864(1995).  
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.  
CC -!- SIMILARITY: Belongs to the pqqC family.  
CC -----  
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CC -----  
DR EMBL; X87299; CAA60734.1; -.  
DR PIR; S58244; S58244.  
DR HAMAP; MF\_00654; -; 1.  
KW PQQ biosynthesis.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 M 6  
|  
Db 1 M 1

# RESULT 53

## PVK1\_PERAM

ID PVK1\_PERAM STANDARD; PRT; 11 AA.  
AC P41837;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Periviscerokinin-1 (Pea-PVK-1).  
OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Abdominal perisymphathetic organs;  
 RX MEDLINE=95232021; PubMed=7716075;  
 RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;  
 RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the  
 RT perisymphathetic organs of the American cockroach."  
 RL Peptides 16:61-66(1995).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE  
 CC HYPERNEURAL MUSCLE.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 2 A 2

#### RESULT 54

RANC\_RANPI  
 ID RANC\_RANPI STANDARD; PRT; 11 AA.  
 AC P08951;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Ranatensin-C.  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=84131098; PubMed=6141890;  
 RA Nakajima T.;  
 RL Unpublished results, cited by:  
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;  
 RL Comp. Biochem. Physiol. 77C:99-108(1984).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin  
 CC family.  
 DR InterPro; IPR000874; Bombesin.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 T 5  
|  
Db 2 T 2

RESULT 55

RRPL\_CHAV

ID RRPL\_CHAV STANDARD; PRT; 11 AA.  
AC P13179;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)  
DE (L protein) (Fragment).  
GN L.  
OS Chandipura virus (strain I653514).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Rhabdoviridae; Vesiculovirus.  
OX NCBI\_TaxID=11273;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89299473; PubMed=2741347;  
RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,  
RA Banerjee A.K.;  
RT "Structure and expression of the glycoprotein gene of Chandipura  
RT virus."  
RL Virology 171:285-290(1989).  
CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE  
CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS  
CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.  
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
CC {RNA} (N).  
CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE  
CC NUCLEOCAPSID (N) PROTEIN.  
CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND  
CC PARAMYXOVIRUSES.  
CC -----  
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CC -----  
DR EMBL; J04350; AAA42917.1; -.  
KW Transferase; RNA-directed RNA polymerase.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 M 6

|

Db 1 M 1

RESULT 56

T2P1\_PROVU

ID T2P1\_PROVU STANDARD; PRT; 11 AA.

AC P31031;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)

DE (R.PvuI) (Fragment).

GN PVUIR.

OS Proteus vulgaris.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Proteus.

OX NCBI\_TaxID=585;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 13315;

RX MEDLINE=93087186; PubMed=1454536;

RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;

RT "Cloning and characterization of genes for the PvuI restriction and

RT modification system.";

RL Nucleic Acids Res. 20:5743-5747(1992).

CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND

CC CLEAVES AFTER T-4.

CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give

CC specific double-stranded fragments with terminal 5'-phosphates.

CC -----  
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CC -----

DR EMBL; L04163; AAA25660.1; -.

DR PIR; S35490; S35490.

DR REBASE; 1541; PvuI.

KW Restriction system; Hydrolase; Nuclease; Endonuclease.

FT NON\_TER 1 1

SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 S 11

|

Db 2 S 2

## RESULT 57

TIN4\_HOPTI

ID TIN4\_HOPTI STANDARD; PRT; 11 AA.  
 AC P82654;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tigerinin-4.  
 OS *Hoplobatrachus tigerinus* (Indian bull frog) (*Rana tigerina*).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
 OC *Hoplobatrachus*.  
 OX NCBI\_TaxID=103373;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
 RC TISSUE=Skin secretion;  
 RX PubMed=11031261;  
 RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,  
 RA Devi A.S., Nagaraj R., Sitaram N.;  
 RT "Tigerinins: novel antimicrobial peptides from the Indian frog *Rana*  
 RT *tigerina*.";  
 RL J. Biol. Chem. 276:2701-2707(2001).  
 CC -!- FUNCTION: Antibacterial activity against *B.subtilis*, *E.coli*,  
 CC *S.aureus*, *M.luteus*, *P.putida* and *S.cerevisiae*.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.  
 KW Amphibian defense peptide; Antibiotic.  
 FT DISULFID 3 11  
 SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2  
 |  
 Db 1 R 1

## RESULT 58

TKC2\_CALVO

ID TKC2\_CALVO STANDARD; PRT; 11 AA.  
 AC P41518;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Callitachykinin II.  
 OS *Calliphora vomitoria* (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95075727; PubMed=7984492;

RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,  
 RA Naessel D.R.;  
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from  
 RT the blowfly, *Calliphora vomitoria*, that have resemblances to  
 RT tachykinins.";  
 RL Peptides 15:761-768(1994).  
 CC -!- FUNCTION: Myoactive peptide.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1  
 |  
 Db 6 A 6

# RESULT 59

## TKN1\_PSEGU

ID TKN1\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42986;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-I (PG-KI).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog *Pseudophryne guentheri*.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; B60409; B60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.



KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

# RESULT 60

## TKN1\_UPEIN

ID TKN1\_UPEIN STANDARD; PRT; 11 AA.  
 AC P82026;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Uperin 1.1.  
 OS Uperoleia inundata (Floodplain toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;  
 OC Myobatrachinae; Uperoleia.  
 OX NCBI\_TaxID=104953;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,  
 RA Adams G.W., Severini C.;  
 RT "Novel uperin peptides from the dorsal glands of the australian  
 RT floodplain toadlet Uperoleia inundata.";  
 RL Aust. J. Chem. 49:475-484(1996).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

RESULT 61

TKN1\_UPERU

ID TKN1\_UPERU STANDARD; PRT; 11 AA.  
AC P08612;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Uperolein.  
OS Uperoleia rugosa (Wrinkled toadlet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyla; Myobatrachidae;  
OC Myobatrachinae; Uperoleia.  
OX NCBI\_TaxID=8368;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=75131227; PubMed=1120493;  
RA Anastasi A., Erspamer V., Endean R.;  
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring  
RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";  
RL Experientia 31:394-395(1975).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR InterPro; IPR008215; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

RESULT 62

TKN2\_PSEGU

ID TKN2\_PSEGU STANDARD; PRT; 11 AA.  
AC P42987;

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-II (PG-KII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guentheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; C60409; C60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

#### RESULT 63

##### TKN3\_PSEGU

ID TKN3\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42988;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Kassinin-like peptide K-III (PG-KIII).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;

OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guntheri.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; D60409; D60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

#### RESULT 64

##### TKN4\_PSEGU

ID TKN4\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42989;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P-like peptide I (PG-SPI).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylloidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,

RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog *Pseudophryne guntheri*.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; E60409; E60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

# RESULT 65

## TKN5\_PSEGU

ID TKN5\_PSEGU STANDARD; PRT; 11 AA.  
 AC P42990;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Substance P-like peptide II (PG-SPII).  
 OS *Pseudophryne guentheri* (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;  
 OC Myobatrachinae; *Pseudophryne*.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,  
 RA Roberts J.D., Melchiorri P., Erspamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog *Pseudophryne guntheri*.";  
 RL Peptides 11:299-304(1990).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth

CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; F60409; F60409.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR InterPro; IPR008215; Tachykinin.  
 DR Pfam; PF02202; Tachykinin; 1.  
 DR SMART; SM00203; TK; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 1 Q 1

#### RESULT 66

##### TKN\_ELEMO

ID TKN\_ELEMO STANDARD; PRT; 11 AA.  
 AC P01293;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Eledoisin.  
 OS Eledone moschata (Musky octopus) (Ozaena moschata), and  
 OS Eledone cirrhosa (Curled octopus) (Ozaena cirrosa).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.  
 OX NCBI\_TaxID=6641, 102876;  
 RN [1]  
 RP SEQUENCE.  
 RA Anastasi A., Erspamer V.;  
 RT "The isolation and amino acid sequence of eledoisin, the active  
 RT endecapeptide of the posterior salivary glands of Eledone.";  
 RL Arch. Biochem. Biophys. 101:56-65(1963).  
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
 CC evoke behavioral responses, are potent vasodilators and  
 CC secretagogues, and contract (directly or indirectly) many smooth  
 CC muscles.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the tachykinin family.  
 DR PIR; A01561; EOOC.  
 DR PIR; B01561; EOCC.  
 DR PDB; 1MXQ; 18-FEB-03.  
 DR InterPro; IPR002040; Tachy\_Neurokinin.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;

KW 3D-structure.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
|  
Db 1 Q 1

RESULT 67

TKN\_PHYFU

ID TKN\_PHYFU STANDARD; PRT; 11 AA.  
AC P08615;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Physalaemin.  
OS Physalaemus fuscumaculatus (Neotropical frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;  
OC Leptodactylinae; Physalaemus.  
OX NCBI\_TaxID=8378;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=66076612; PubMed=5857249;  
RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;  
RT "Structure and pharmacological actions of physalaemin, the main  
RT active polypeptide of the skin of Physalaemus fuscumaculatus.";  
RL Experientia 20:489-490(1964).  
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,  
CC evoke behavioral responses, are potent vasodilators and  
CC secretagogues, and contract (directly or indirectly) many smooth  
CC muscles.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the tachykinin family.  
DR PIR; S07201; S07201.  
DR InterPro; IPR002040; Tachy\_Neurokinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3

Db                    |  
                      1 Q 1

RESULT 68

UF05\_MOUSE

ID    UF05\_MOUSE            STANDARD;            PRT;        11 AA.  
AC    P38643;  
DT    01-OCT-1994 (Rel. 30, Created)  
DT    01-OCT-1994 (Rel. 30, Last sequence update)  
DT    15-MAR-2004 (Rel. 43, Last annotation update)  
DE    Unknown protein from 2D-page of fibroblasts (P48) (Fragment).  
OS    Mus musculus (Mouse).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX    NCBI\_TaxID=10090;  
RN    [1]  
RP    SEQUENCE.  
RC    TISSUE=Fibroblast;  
RX    MEDLINE=95009907; PubMed=7523108;  
RA    Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT    "Separation and sequencing of familiar and novel murine proteins  
RT    using preparative two-dimensional gel electrophoresis."  
RL    Electrophoresis 15:735-745(1994).  
CC    -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC    protein is: 5.5, its MW is: 48 kDa.  
FT    NON\_TER            11        11  
SQ    SEQUENCE    11 AA;    1328 MW;    E54835E5CAAABAFa CRC64;

Query Match                    9.1%;    Score 1;    DB 1;    Length 11;  
Best Local Similarity    100.0%;    Pred. No. 1e+05;  
Matches        1;    Conservative        0;    Mismatches        0;    Indels        0;    Gaps        0;

QY                    4 K 4  
                      |  
Db                    1 K 1

RESULT 69

ULAG\_HUMAN

ID    ULAG\_HUMAN            STANDARD;            PRT;        11 AA.  
AC    P31933;  
DT    01-JUL-1993 (Rel. 26, Created)  
DT    01-JUL-1993 (Rel. 26, Last sequence update)  
DT    15-MAR-2004 (Rel. 43, Last annotation update)  
DE    Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).  
OS    Homo sapiens (Human).  
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX    NCBI\_TaxID=9606;  
RN    [1]  
RP    SEQUENCE.  
RC    TISSUE=Liver;  
RX    MEDLINE=94147969; PubMed=8313870;  
RA    Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
RA    Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
RT    "Human liver protein map: update 1993.";



RL Electrophoresis 14:1216-1222(1993).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 5.5, its MW is: 34 kDa.  
 DR SWISS-2DPAGE; P31933; HUMAN.  
 DR Siena-2DPAGE; P31933; -.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 Q 3  
 |  
 Db 3 Q 3

# RESULT 70

## RE41\_LITRU

ID RE41\_LITRU STANDARD; PRT; 11 AA.  
 AC P82074;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Rubellidin 4.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylinae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australin red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians."  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
 CC activity.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 0.0%; Score 0; DB 1; Length 11;  
 Best Local Similarity 0.0%; Pred. No. 1.4e+05;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 A 1  
 Db 1 G 1

Search completed: April 8, 2004, 15:47:20  
Job time : 5.15385 secs